

```

Db 475 CPTSKKEQPGQEELOPPPR-----TETTELSPPPARPKPSAELLQRYSP----- 520
QY 52 TGLFGEDVFRFSAPVYM-----PTWVLRRTPACAGRSVYTEAY-----VTIPV 96
Db 521 -----KKQVRIASPVMOERRELCPQLPPRGSPITLDGSSSPTNAVSGPKKPLPLPI 575
QY 97 GCTCVPEPEKADDSINSSIDKOGAKLLLGPNDA 130
Db 576 ACR--PRPSNGVNSPNS-----SPGSAP 597

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RESULT 15

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O46545
ID O46545 PRELIMINARY; PRT; 1045 AA.
AC O46545;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE COMPLEMENT RECEPTOR TYPE 2.
GN CR2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-WHITE ALPINE;
RA Hein W.R., Dudler L., Marston W., Landsverk T., Young A., Avila D.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF038131; AAB92375.1; -.
DR HSSP; P10998; LVVD.
DR InterPro; IPR000436; -.
DR Pfam; PF00084; sush1; 14.
DR SMART; SM00032; CCP; 1.
SQ SEQUENCE 1045 AA; 115561 MW; FF58E1A2892C0D59 CRC64;

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Query Match 10.6%; Score 77.5; DB 6; Length 1045;
Best Local Similarity 25.9%; Pred. No. 8.7;
Matches 29; Conservative 13; Mismatches 43; Indels 27; Gaps 5;

QY 15 PPTNLRSPWYRISYDPARYPLPEAYLCRGCLTG--LFGEEDVFRFSAPVYMPV 72
Db 423 PPKILNGQKEDRHRVDFDPTGSIRY-----SCDPGYVLVGEESIRCTPDGVMIPTA 473
QY 73 VLRRTPACAGRSVYTEAYVTIPVGCVCVPEPEK--ADSINSSIDKOGAKL 122
Db 474 PICKAACEB-----PVGKQVFKPKNQFIRPDVNSSCD-EGYRL 511

```

Search completed: October 5, 2001, 15:23:45  
Job time: 190 sec



[illegible]

## RESULT 7

	Query Match	15.28;	Score 110.5;	DB 4;	Length 177;
	Best Local Similarity	31.5%;	Pred. No. 0.00036;		
	Matches	29;	Conservative 11;	Mismatches 45;	Indels 7; Gaps 3
Qy	16	PTNLRKSPWYAIRSYDPAARYPRYLPELCAICRGCLTGLFGEE-DVRFPSAPVYMPTVVL	74		
		:        :	:	:	
Db	81	PLNSRAITSPRWELDRDLNRLLPQDIYHARCLCPHCVSILQTGSHMDPRGNSELLYHNQTVF	140		
		:	:	:	
Qy	75	RRTFACAGRSVY-----TEAYVIIPVGCTCV	101		
		:	:	:	
Db	141	YRRP-CHGEKGTHRGYCLERRLRYRVSACVCV	171		

DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	
DE	CYTOKINE-LIKE PROTEIN ZCYT07 (INTERLEUKIN 20) (INTERLEUKIN 17B)	
DE	(NEURONAL INTERLEUKIN-17 RELATED FACTOR) (INTERLEUKIN-17 BETA).	
GN	ZCYT07 OR IL20.	
OS	Homo sapiens (human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
EN	SEQUENCE FROM N.A.	
RA	Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,	
RA	Martinez T., Hoffman R., O'Hara P.;	
RL	Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20317118; PubMed=10749887;	
RA	Shi Y., Ullrich S.J., Zhang J., Connolly K., Grzegorzewski K.J.,	
RA	Barber M.C., Wang W., Wathen K., Hodge V., Fisher C.L., Olsen H.,	
RA	Ruben S.M., Knyazev I., Cho Y.H., Kao V., Wilkinson K.A.,	
RA	Carrell J.A., Ebner R.;	
RT	"A novel cytokine receptor-ligand pair. Identification, molecular	
RT	characterization, and in vivo immunomodulatory activity.";	
RL	J. Biol. Chem. 275:19167-19176(2000).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=20105548; PubMed=10639155;	
RA	Li H., Chen J., Huang A., Stinson J., Heldens S., Foster J., Dowd P.,	
RA	Gurney A.L., Wood W.I.;	
RT	"Cloning and Characterization of IL-17B and IL17C, Two New Members of	
RT	the IL-17 Cytokine Family.";	
RL	Proc. Natl. Acad. Sci. U.S.A. 97:773-778(2000).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RA	Moore E.E., Presnell S., Garrigues U., Guilbot A., LeGuern E.,	
RA	Smith D., Yao L., Whitmore T.E., Gilbert T., Kuestner R.E.;	
RT	"Identification of a novel IL-17 related factor: Demonstration of	
RT	neuronal expression and evaluation as a candidate for the chromosome	
RT	5q-linked form of Charcot-Marie-Tooth disease.";	
RL	Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.	
RN	[5]	
RP	SEQUENCE FROM N.A.	
RA	Zhang W., Wang J., Cao X.;	
RT	"Novel cytokine homology with interleukin-17.";	
RL	Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AF184569; AAF01318.1; -	
DR	EMBL: AF212311; AAF78775.1; -	
DR	EMBL: AF152098; AAF28104.1; -	
DR	EMBL: AF218727; AAG44136.1; -	
DR	EMBL: AF110385; AAG39637.1; -	
SQ	SEQUENCE 180 AA; 20437 MW; F1B0BC1446D0B14A CRC64;	
Query Match 23.9%; Score 174; DB 4; Length 180;		
Best Local Similarity 43.7%; Pred. No. 6e-11;		
Matches 38; Conservative 9; Mismatches 38; Indels 2; Gaps		
QY	17 TNLRSVSPWAFRISYDARYPRYLPEAVCLRCGLCTGLFGEEDVRFPSAPVMTVVLRR 76	
Db	:   :     :     :     :     :     :     :     :     :	
QY	93 SNKRSLSFGWYSINHDPSRIPDPEARCLCLGCVNFTWOEDRSWVSVPFVSQVPPVRR 151	
Db	:   :     :     :     :     :     :     :     :	
QY	77 --TPACAGGRSVYTEAYVTVPVGTCTV 101	
Db	:   :     :     :     :     :     :     :     :	
QY	153 LCPFPPTGTCRQAVMETIAGVCTCI 179	
Db	:   :     :     :     :     :     :     :     :	
RESULT	5	
Q9QXT6	PRELIMINARY; PRT; 180 AA.	
ID	Q9QXT6	
AC	Q9QXT6	
DT	01-MAY-2000 (TrEMBLrel. 13, Created)	
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)	
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)	

Result No.	Score		Query Match	Length	DB	ID	Description
	Score	Match					
1	187.5	25.7	197	4	Q9P0M4	Q9P0M4	homo sapien
2	187.5	25.7	197	4	Q9HC75	Q9HC75	homo sapien
3	176.5	24.2	178	11	Q9EQ16	Q9EQ16	mesocricetu
4	174	23.9	180	4	Q9UH5	Q9UH5	homo sapien
5	173	23.7	180	11	Q9QXT6	Q9QXT6	mus musculus
6	151	20.7	111	11	Q9EQ17	Q9EQ17	rattus norv
7	119.5	16.4	78	4	Q9NUE6	Q9NUE6	homo sapien
8	110.5	15.2	177	4	Q9H293	Q9H293	homo sapien
9	107.5	14.7	151	14	Q4O633	Q4O633	salmirline
10	99	13.6	148	5	Q19778	Q19778	caenorhabdi
11	79.5	10.9	520	4	Q9UBG7	Q9UBG7	homo sapien
12	78.5	10.8	226	5	Q9XUH9	Q9XUH9	caenorhabdi
13	78	10.7	552	4	Q95723	Q95723	homo sapien
14	78	10.7	805	5	Q9VED4	Q9VED4	drosophila
15	77.5	10.6	1045	6	Q46545	Q46545	ovis aries
16	76	10.4	242	2	Q9PL24	Q9PL24	chlamydia m
17	75.5	10.4	509	10	Q48780	Q48780	arabidopsis m
18	75	10.3	178	2	Q9X0U1	Q9X0U1	thermotoga
19	75	10.3	242	2	Q94019	Q94019	chlamydia t

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Db	24	ACCLDGRPPIVPHRRRRRIIAALRSVLRMRDTPRARSQCDOVTSHAVLLIGHNRPVRRHGG	83
Qy	39	YLPAYCLCRGC-----LTGLEGEEDVR-----FRSAPVYMTPTVVLRTTACAGG----	83
Db	84	ELPRGALALGICALLLMGIVGCTTVDGTAMPDPTNVAPRYSVSASVSAATSSIRE	14
Qy	84	-----RSVYTEAYVIVPGCTCVPEPKDA-DSINSSIDKQAKLLLGENDAPA	131
Db	144	SROOSLTTTKA---IRTSQDALAATSKDAIDKVNAYVAAFNQGRNTGTGTEGPA	193

```

RESULT 14
TTP_BOVIN
ID TTP_BOVIN STANDARD; PRT; 324 AA.
AC P53781;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE TRISTRAPOLINE (TTP) (TISLIA PROTEIN) (TISLI) (ZFP-36).
OS ZFP36.
OS Bos taurus (Bovine).

```

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
OX NCBI\_TaxID=9913;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RC MEDLINE=96027638; PubMed=7559666;  
RX Lai W.S., Thompson M.J., Taylor G.A., Liu Y., Blackshear P.J.:  
RA "Promoter analysis of zfp-36, the mitogen-inducible gene encoding the  
RT zinc finger protein tristetraprolin.";  
RT J. Biol. Chem. 270:25266-25272(1995).  
CC -I- FUNCTION: PROBABLE REGULATORY PROTEIN WITH A NOVEL ZINC FINGER  
CC STRUCTURE INVOLVED IN REGULATING THE RESPONSE TO GROWTH FACTORS.  
CC

```

CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- INDUCTION: BY STIMULATION WITH VARIOUS MITOGENS.
CC -!- SIMILARITY: CONTAINS 2 CX(8)CX(5)CX(3)H-TYPE ZINC FINGERS.
CC -----
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CC -----
CC DR EMBL; L42319; AAB05819.1; -.
CC DR InterPro; IPR000571; -.
CC DR Pfam; PF00642; zf-CCCH; 2.

```

KW	Nuclear protein; Repeat; Metal-binding; Zinc-finger; DNA-binding.	
FT	REPEAT	69 73 P-P-P-P-G.
FT	REPEAT	196 200 P-P-P-P-G.
FT	REPEAT	218 222 P-P-P-P-G.
FT	ZN_FING	107 126 CX(8)CX(5)CX(3)H-TYPE.
FT	ZN_FING	145 164 CX(8)CX(5)CX(3)H-TYPE.
SQ	SEQUENCE	324 AA; 34087 MW; 6046057E9EA278EE CRC64;
Query Match 9.5%; Score 69.5; DB 1; Length 324;		
Best Local Similarity 28.0%; Pred. No. 3.9;		
Matches 42; Conservative 10; Mismatches 51; Indels 47; Gaps		
QV	6 GRPADRRR-PPTNLR--SVSPWRYRISYDPAARYPRYL---PEAYCLRCRGCLTGLGFGEED 59	

[illegible]

DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DE 01-OCT-2000 (Rel. 40, Last annotation update)  
DE CYCLIN-DEPENDENT KINASE INHIBITOR 1 (MELANOMA DIFFERENTIATION  
DE ASSOCIATED PROTEIN 6) (MDA-6) (p21) (CDK-INTERACTING PROTEIN 1).  
GN CDKN1A OR CDKN1 OR CIP1 OR WAF1 OR MDA6 OR SD11 OR P131 OR CAP20.  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE-94061996; PubMed-8242751;  
RX Harper J.W., Adami G.R., Wei N., Keyomarsi K., Ellledge S.J.;  
RA "The p21 Cdk-Interacting protein Cipl is a potent inhibitor of G1  
RT cyclin-dependent kinases.";  
RL Cell 75:805-816(1993).  
RN [2]  
RP MEDLINE-94061997; PubMed-8242752;  
RX El-Deiry W.S., Tokino T., Velculescu V.E., Levy D.B., Parsons R.,  
RA Trent J.M., Lin D., Mercer W.E., Kinzler K.W., Vogelstein B.;  
RT "WAF1, a potential mediator of p53 tumor suppression.";  
RL Cell 75:817-825(1993).  
RN [3]  
RP MEDLINE-94081955; PubMed-8259214;  
RX Xiong Y., Hannon G.J., Zhang H., Casso D., Kobayashi R., Beach D.;  
RA "p21 is a universal inhibitor of cyclin kinases.";  
RL Nature 366:701-704(1993).  
RN [4]  
RP MEDLINE-94170884; PubMed-8125163;  
RX Noda A., Ning Y., Venable S.F., Pereira-Smith O.M., Smith J.R.;  
RA "Cloning of senescent cell-derived inhibitors of DNA synthesis using  
RT an expression screen.";  
RL Exp. Cell Res. 211:90-98(1994).  
RN [5]  
RP MEDLINE-95384154; PubMed-7655464;  
RX Mouses S., Oezcelik H., Lee P.D., Malkin D., Bull S.B.,  
RA Andrusis I.L.;  
RT "Two variants of the CIP1/WAF1 gene occur together and are associated  
RT with human cancer.";  
RL Hum. Mol. Genet. 4:1089-1092(1995).  
RN [6]  
RP MEDLINE-97015085; PubMed-8861913;  
RX Gulbis J.M., Keinan Z., Hurwitz J., O'Donnell M., Kuriyan J.;  
RA "Structure of the C-terminal region of p21(WAF1/CIP1) complexed with  
RT human PCNA.";  
RL Cell 87:297-306(1996).  
CC -1- FUNCTION: MAY BE THE IMPORTANT INTERMEDIATE BY WHICH P53 MEDIATES  
CC ITS ROLE AS AN INHIBITOR OF CELLULAR PROLIFERATION IN RESPONSE TO  
CC DNA DAMAGE. MAY BIND TO AND INHIBIT CYCLIN-DEPENDENT KINASE  
CC ACTIVITY, PREVENTING PHOSPHORYLATION OF CRITICAL CYCLIN-DEPENDENT  
CC KINASE SUBSTRATES AND BLOCKING CELL CYCLE PROGRESSION.  
CC -1- SUBCELLULAR LOCATION: NUCLEAR.

CC -1- TISSUE SPECIFICITY: IS EXPRESSED IN ALL ADULT HUMAN TISSUES,  
CC WITH 5-FOLD LOWER LEVELS OBSERVED IN THE BRAIN.  
CC -1- INDUCTION: BY THE P53 TUMOR SUPPRESSOR/ONCOGENE. ALSO BY MEZEREIN  
CC (ANTILEUKEMIC COMPOUND) AND BY IFN-BETA.  
CC -1- SIMILARITY: THE N-TERMINAL OF CIP1 AND KIP ARE SIMILAR.  
CC  
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CC  
CC EMBL; L25610; AAA16109.1; -  
CC EMBL; S67388; AAB29246.1; -  
CC EMBL; U09579; AAB85641.1; -  
CC EMBL; U03106; AAC04313.1; -  
CC EMBL; L26165; AAA19811.1; -  
CC EMBL; L47233; AAB59560.1; ALT\_INIT.  
CC EMBL; Z85996; CAB06656.1; -  
CC PIR; S39357; S39357.  
CC SWISS-2DPAGE; P38936; HUMAN.  
CC MIM; 116899; -  
KW Cell cycle; Nuclear protein; Zinc-finger.  
FT ZN\_FING 13 41 C4-TYPE (POTENTIAL).  
FT DOMAIN 141 156 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).  
SQ SEQUENCE 164 AA; 18119 MW; 98D1E7C519ADFCA9 CRC64;  
Query Match 9.8%; Score 71.5; DB 1; Length 164;  
Best Local Similarity 25.2%; Pred. No. 1.1;  
Matches 39; Conservative 10; Mismatches 53; Indels 53; Gaps 6;  
QY 3 PAG-----GRPADRRFRPTNLRVSVPWAYRISYDPARYPRYLPEAYCLCRG----- 50  
DB 4 PAGDVQRNFCGSKACRRLFGPVDSEQLS-----RDCDALMAGCIQEAR 46  
QY 51 -----ITGLFGEDVFRFSAP-VYMTVVVLRRTACAGGRSVYT----- 88  
DB 47 ERWNFDFVTETPLEGDFAWERVRLGLPKLYLPTGPRGRDELGGRRRPTSPALLOGTA 106  
QY 89 -EAYVTIPGCTCVPEPEKAD-SINSSIDKQAK 121  
DB 107 EEDHVDLSLCTLVPRSGEQAEGSGPGDGSQGRK 141  
RESULT 12  
Y450\_HUMAN  
ID Y450\_HUMAN STANDARD; PRT; 425 AA.  
AC 075038;  
DT 01-OCT-2000 (Rel. 40, Created)  
DT 01-OCT-2000 (Rel. 40, Last sequence update)  
DE 01-OCT-2000 (Rel. 40, Last annotation update)  
DE HYPOTHETICAL PROTEIN KIAA0450.  
GN KIAA0450  
OS Homo sapiens (human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE-98116662; PubMed-9455484;  
RA Seki N., Ohira M., Nagase T., Ishikawa K.-I., Miyajima N.,  
RA Nakajima D., Nomura N., Ohara O.;  
RT "Characterization of cDNA clones in size-fractionated cDNA libraries  
RT from human brain.";  
RL DNA Res. 4:345-349(1997).  
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KW Glycoprotein; Blood coagulation; Plasma; Kringle; Serine protease;  
 KW Hydrolase; Fibrinolysis; EGF-like domain; Repeat; Zymogen; Signal.

FT SIGNAL 1 1  
 FT CHAIN 19 358 ALPHA-FACTOR XIIA HEAVY CHAIN.  
 FT CHAIN 359 603 ALPHA-FACTOR XIIA LIGHT CHAIN.  
 FT DOMAIN 46 87 FIBRONECTIN TYPE-II.  
 FT DOMAIN 93 130 EGF-LIKE 1.  
 FT DOMAIN 132 172 FIBRONECTIN TYPE-I.  
 FT DOMAIN 173 209 EGF-LIKE 2.  
 FT DOMAIN 216 294 KRINGLE.  
 FT DOMAIN 342 342 PRO-RICH.  
 FT DOMAIN 359 603 CATALYTIC.  
 FT ACT\_SITE 398 398 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 447 447 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT ACT\_SITE 551 551 CHARGE RELAY SYSTEM (BY SIMILARITY).  
 FT DISULFID 97 109 BY SIMILARITY.  
 FT DISULFID 103 118 BY SIMILARITY.  
 FT DISULFID 120 129 BY SIMILARITY.  
 FT DISULFID 134 162 BY SIMILARITY.  
 FT DISULFID 160 169 BY SIMILARITY.  
 FT DISULFID 177 188 BY SIMILARITY.  
 FT DISULFID 182 197 BY SIMILARITY.  
 FT DISULFID 199 208 BY SIMILARITY.  
 FT DISULFID 216 294 BY SIMILARITY.  
 FT DISULFID 237 276 BY SIMILARITY.  
 FT DISULFID 265 289 BY SIMILARITY.  
 FT DISULFID 345 472 BY SIMILARITY.  
 FT DISULFID 383 399 BY SIMILARITY.  
 FT DISULFID 391 461 BY SIMILARITY.  
 FT DISULFID 422 425 BY SIMILARITY.  
 FT DISULFID 488 557 BY SIMILARITY.  
 FT DISULFID 520 536 BY SIMILARITY.  
 FT DISULFID 547 578 BY SIMILARITY.  
 FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 270 270 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 419 419 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 603 AA; 66795 MW; 48DC6B946FB9ED59 CRC64;

Query Match 10.3%; Score 75; DB 1; Length 603;  
 Best Local Similarity 22.2%; Pred. No. 2.1;  
 Matches 37; Conservative 17; Mismatches 59; Indels 54; Gaps 7;

QY 2 CPAGGRPADRRPRPT-NLRVSPWAYRISVDPRYPY-----LPEAY 44  
 DB 60 CIHKGRGPRWCATPNPDQDQWYCL--EPKKVKDCSKHNPQCGGICVNTLSSPH 117

QY 45 CLCRGLTG-----LFGEEDVFRSAPV-----YMPYVL 74  
 DB 118 CLCPDLTKGKHCOREKCFEPQLHRRFFHENEIWFRTGPAGVAKCHCKGPDHCKQMHSQEC 177

QY 75 RTRPACAGRSVYTRAY--VTIPVGCTCVPEPEKDAADSIINSIDKQG 119  
 DB 178 QTNPCNLNGRCLEVEGHILDCPMGYT---GPFCDLDTTASCYEGRG 221

RESULT 8  
 YAR2\_SCHPO STANDARD; PRT; 1273 AA.  
 AC Q10135;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last annotation update)  
 DE HYPOTHETICAL 142.5 KDA PROTEIN C23E2.02 IN CHROMOSOME I.  
 GN SPAC23E2.02.  
 OS Schizosaccharomyces pombe (fission yeast).  
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
 OC Schizosaccharomycetes.  
 OX NCBI\_TaxID=4896;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN=972;  
 RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;  
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.  
 CC -----  
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 CC -----  
 CC EMBL: Z68887; CAA93114.1; .  
 DR InterPro: IPR002937; .  
 DR Pfam: PF01593; Amino\_oxidase; 1.  
 DR Hypothetical protein; Transmembrane.  
 KW TRANSMEM 1028 1048 POTENTIAL.  
 FT TRANSMEM 1273 AA; 142489 MW; 3FEFF6433DF3C0B6 CRC64;  
 SQ SEQUENCE 1273 AA; 142489 MW; 3FEFF6433DF3C0B6 CRC64;

Query Match 10.2%; Score 74.5; DB 1; Length 1273;  
 Best Local Similarity 25.6%; Pred. No. 5.4;  
 Matches 22; Conservative 15; Mismatches 48; Indels 1; Gaps 1;

QY 46 LCRGLTGLFGEEDVFRSAPVYMPYVTRTPACAGRSVYTRAYTIPVGCTCVPEPE 105  
 DB 520 ICARQLTGLFSQYSSFLSKNELPKVILEAKERTGGR-IYSRALPVSHTSATQINHT 578

QY 106 KDAISINSIDKQAKLLGPNDA 131  
 DB 579 SNSNSISNSTSLNPKDVTDP SHIPS 604

RESULT 9

CR2\_HUMAN  
 ID CR2\_HUMAN STANDARD; PRT; 1033 AA.  
 AC P20023;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE COMPLEMENT RECEPTOR TYPE 2 PRECURSOR (CR2) (COMPLEMENT C3D RECEPTOR)  
 DE (EPSTEIN-BARR VIRUS RECEPTOR) (EBV RECEPTOR) (CD21 ANTIGEN).  
 GN CR2 OR C3DR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89123277; PubMed=2563370;  
 RA Fujisaku A., Harley J.B., Frank M.B., Gruner B.A., Frazier B.,  
 RA Holers V.M.;  
 RT "Genomic organization and polymorphisms of the human C3d/Epstein-Barr  
 RT virus receptor.";  
 RL J. Biol. Chem. 264:2118-2125(1989).  
 RN [2]  
 RP SEQUENCE OF 226-233; 256-267; 332-341; 667-677 AND 898-908.  
 RX MEDLINE=86287311; PubMed=3016712;  
 RA Weis J.J., Fearon D.T., Klickstein L.B., Wong W.W., Richards S.A.,  
 RA de Bruyn Kops A., Smith J.A., Weis J.H.;  
 RT "Identification of a partial cDNA clone for the C3d/Epstein-Barr  
 RT virus receptor of human B lymphocytes: homology with the receptor for  
 RT fragments C3b and C4b of the third and fourth components of  
 RT complement.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 83:5639-5643(1986).  
 RN [3]  
 RP SEQUENCE OF 492-556 FROM N.A. (SHORT ISOFORM).  
 RX MEDLINE=93294286; PubMed=8390533;  
 RA Sinha S.K., Todd S.C., Hedrick J.A., Speiser C.L., Lambiris J.D.,  
 RA Tsoukas C.D.;  
 RT "Characterization of the EBV/C3d receptor on the human Jurkat T cell  
 RT line: evidence for a novel transcript.";  
 RL J. Immunol. 150:5311-5320(1993).



```

SQ SEQUENCE 150 AA; 16876 MW; EF13F33EDFD9D689F CRC64;

Query Match 14.8%; Score 108; DB 1; Length 150;
Best Local Similarity 34.4%; Pred. No. 0.00013;
Matches 31; Conservative 11; Mismatches 42; Indels 6; Gaps 4;

QY 14 RPPTNL-RVSPWAYRISYPARYPRYLPEAYCLRCGLTGLFGDEEDVRFRSAPVYMPVT 72
   || || || | : || || | : || | : | : | : | : | : | : | : | : | :
Db 57 RPSDYLNRSPTWLSRNEPDRYPSVIWEAQCRHQRVCNA-BGKLDHHMNSVLIOQEIL 115
   || || | : || || | : || | : | : | : | : | : | : | : | : | :

QY 73 VLRRTP-ACAGGRSVYTEAVYTIPVGCTCV 101
   || || | : || || | : || || | : || || | : || || | : || || | : || || | :
Db 116 VLKREPKCP---FTFRVKMLGVGCGTCV 142

RESULT 5
THIC_RHIET STANDARD; PRT; 610 AA.
ID THIC_RHIET ID THIC_RHIET
AC O34291;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE THIAMINE BIOSYNTHESIS PROTEIN THIC.
GN THIC.
OS Rhizobium etli.
OG Plasmid pb.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBI_TaxID=29449;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CE3.
RY MEDLINE=98037482; PubMed=9371431;
RA Miranda-Rios J., Morera C., Taboada H., Dávalos A., Encarnacion S.,
RD Mora J., Soboron M.;
RT "Expression of thiamin biosynthetic genes (thiCOGE) and production of
RL symbiotic terminal oxidase cbb3 in Rhizobium etli.";
RL J. Bacteriol. 179:6887-6893(1997).
CC -1- FUNCTION: REQUIRED FOR THE SYNTHESIS OF THE HYDROMETHYLPYRIMIDINE
      (HMP) MOIETY OF THIAMINE (4-AMINO-2-METHYL-5-
      HYDROXYMETHYLPYRIMIDINE) (BY SIMILARITY).
CC -1- PATHWAY: THIAMINE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE THIC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF0044408; AAC45972.1; -.
DR InterPro; IPR002817; -.
DR Pfam; PF01964; ThiC; 1.
KW Thiamine biosynthesis; Plasmid.
SQ SEQUENCE 610 AA; 67105 MW; 9CE7F560DB35ACDC CRC64;

Query Match 10.4%; Score 75.5; DB 1; Length 610;
Best Local Similarity 29.9%; Pred. No. 1.8;
Matches 38; Conservative 14; Mismatches 54; Indels 21; Gaps 7;

QY 3 PAGGRPADDRFRPPTNLRVSPW---AYRISYDPARYPYRLPEAYCLRCGLTGFLGEE-- 57
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 44 PTSGEPI-----PVTVDSSGPYTDPAHVTSID-AGLPR-LRESWIKAARGDVESYDGRIV 95
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

QY 58 --EDVRFERSAPVYMPVTVLLRTPACA--GGRSVYTEAVYTIPVGCTCVPEPEKDADSINS 114
   || || | : || || | : || || | : || || | : || || | : || || | : || || | :
Db 96 KPENDINGATGERLTPEPFVRNTPLKAKAGRAGVTLAYAR-----AGIVTFEMEFIAIREN 150
   || || | : || || | : || || | : || || | : || || | : || || | : || || | :

QY 115 IDKOGAK 121

```





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 5, 2001, 15:20:15 ; Search time 11.55 Seconds  
(without alignments)  
394.457 million cell updates/sec

Title: US-09-320-713-4\_COPY\_28\_160

Perfect score: 729

Sequence: 1 SCPAGGRPADRRFRPTNLR.....SIDKQAKLLLPNDAPAGP 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	130.5	17.9	155	1 IL17_HUMAN	Q16552 homo sapien
2	113.5	15.6	158	1 IL17_MOUSE	Q62386 mus musculu
3	108.5	14.9	151	1 VG13_HSVSA	P24916 herpesvirus
4	108	14.8	150	1 IL17_RAT	Q61453 rattus norv
5	75.5	10.4	610	1 THIC_RHET	O34291 rhicobulum e
6	75	10.3	362	1 A2HS_PIG	P29700 sus scrofa
7	75	10.3	603	1 FA12_CAVPO	Q40962 cavia porce
8	74.5	10.2	1273	1 YAR2_SCHPO	Q10135 schizosacch
9	73.5	10.1	1033	1 CR2_HUMAN	P20023 homo sapien
10	73	10.0	3358	1 PGCY_MOUSE	Q62059 mus musculu
11	71.5	9.8	164	1 CDNL_HUMAN	P38936 homo sapien
12	71.5	9.8	425	1 Y450_HUMAN	O75038 homo sapien
13	70.5	9.7	265	1 YM40_MYCTU	Q10522 mycobacteri
14	69.5	9.5	324	1 TTP_BOVIN	P53781 bos taurus
15	69.5	9.5	1896	1 RPBI_DROME	P04052 drosophila
16	68.5	9.4	191	1 MOBA_RHOCA	O9x7k0 rhodobacter
17	68.5	9.4	342	1 HXCA_MOUSE	P31257 mus musculu
18	68.5	9.4	1075	1 NFC3_MOUSE	P97305 mus musculu
19	67.5	9.3	298	1 MYOD_CHICK	P16075 gallus gall
20	67.5	9.3	384	1 DUS9_HUMAN	O99956 homo sapien
21	67	9.2	2273	1 HFAL_YEAST	P32874 saccharomyc
22	66.5	9.1	1117	1 TCF8_MOUSE	O64318 mus musculu
23	66	9.1	676	1 DNLG_THETH	P26996 thermus aqu
24	65.5	9.0	170	1 PLGE_HUMAN	P49763 homo sapien
25	65.5	9.0	500	1 STCL_EMENI	Q00707 escherichia
26	65	8.9	345	1 YJUN_ECOLI	P39400 escherichia
27	65	8.9	376	1 METK_AQUAE	O67222 aquifex aeo
28	65	8.9	802	1 ACSB_ACEXY	P37716 acetobacter
29	64.5	8.8	285	1 HXA4_MOUSE	P06798 mus musculu
30	64.5	8.8	342	1 HXCA_HUMAN	O9nyd6 homo sapien
31	64.5	8.8	374	1 RLIG_BPT4	P00971 bacteriophag
32	64	8.8	277	1 HXDB_NOTVI	P31263 notophthalm
33	64	8.8	286	1 PYRL_SYNEL	P50034 synechococc

34	64	8.8	497	1 CPDH_MACFA	Q29488 macaca fasc
35	64	8.8	3396	1 PGCY_HUMAN	P13611 homo sapien
36	63.5	8.7	419	1 IRF3_MOUSE	P70671 mus musculu
37	63.5	8.7	429	1 ELK1_MOUSE	P41969 mus musculu
38	63.5	8.7	521	1 DRTS_TRYCR	Q27793 trypanosoma
39	63.5	8.7	649	1 KPCI_APLCA	Q16974 aplysia cal
40	63.5	8.7	1170	1 DP3A_TREPA	O83675 treponema p
41	63	8.6	347	1 FOS_CYPCA	P79702 cyprinus ca
42	62.5	8.6	153	1 NEUV_FUGRU	O42499 fugu rubrip
43	62.5	8.6	262	1 MI43_MYCIT	Q03490 mycobacteri
44	62.5	8.6	322	1 SUCA_CAEBL	P53596 caenorhabdi
45	62.5	8.6	329	1 TAL_MOUSE	P22091 mus musculu

## ALIGNMENTS

RESULT	1
IL17_HUMAN	
ID	IL17_HUMAN
AC	O16552;
DT	01-NOV-1997 (Rel. 35, Created)
DT	01-NOV-1997 (Rel. 35, Last sequence update)
DT	01-OCT-2000 (Rel. 40, Last annotation update)
DE	INTERLEUKIN-17 PRECURSOR (IL-17) (CYTOTOXIC T LYMPHOCYTE-ASSOCIATED
DE	ANTIGEN 8) (CTLA-8).
GN	IL17 OR CTLA8.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=96281911; PubMed=8676080;
RA	Fossiez F., Djossou O., Chomarat P., Flores-Romo L., Ait-Yahia S.,
RA	Maat C., Pin J.-J., Garrone P., Garcia E., Saeland S., Blanchard D.,
RA	Gaillard C., Das Mahapatra B., Rouvier E., Golstein P., Banchereau J.,
RA	Lebecque S.;
RT	"T cell interleukin-17 induces stromal cells to produce
RT	proinflammatory and hematopoietic cytokines.";
J.	J. Exp. Med. 183:2593-2603(1996).
RL	[2]
RP	SEQUENCE FROM N.A.
RC	TISSUE="T-cell;"
RX	MEDLINE=96034436; PubMed=7499828;
RA	Yao Z., Painter S.L., Fanslow W.C., Ulrich D., Macduff B.M.,
RA	Spriggs M.K., Armitage R.J.;
RT	"Human IL-17: a novel cytokine derived from T cells.";
RL	J. Immunol. 155:5483-5486(1995).
CC	-I- FUNCTION: INDUCES STROMAL CELLS TO PRODUCE PROINFLAMMATORY AND
CC	HEMATOPOIETIC CYTOKINES. ENHANCES THE SURFACE EXPRESSION OF THE
CC	INTRACELLULAR ADHESION MOLECULE-1 (ICAM-1) IN FIBROBLASTS.
CC	-I- SUBUNIT: HOMODIMER.
CC	-I- SUBCELLULAR LOCATION: SECRETED.
CC	-I- TISSUE SPECIFICITY: RESTRICTED TO ACTIVATED MEMORY T-CELLS.
CC	-I- PTM: FOUND BOTH IN GLYCOSYLATED AND NONGLYCOSYLATED FORMS.
CC	-I- SIMILARITY: STRONG, TO OTHER MAMMALIAN INTERLEUKIN-17 AND TO
CC	HERPESVIRUS SAIMIRI IMMEDIATE EARLY GENE I3 PROTEIN.
CC	-----
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC	-----
DR	EMBL; Z58820; CAA91233.1; -
DR	EMBL; U32659; AAC50341.1; -
DR	MIM; 603149; -
KW	Cytokine; Glycoprotein; T-cell; Antigen; Signal.
FT	SIGNAL 1 23 POTENTIAL.
FT	CHAIN 24 155 INTERLEUKIN-17.



Search completed: October 5, 2001, 15:20:33  
Job time: 43 sec

A71568  
 hypothetical protein CT016 - Chlamydia trachomatis (serotype D, strain UW3/Cx)  
 C:Species: Chlamydia trachomatis  
 C>Date: 13-Sep-1998 #sequence\_revision 13-Sep-1998 #text\_change 08-Oct-1999  
 C:Accession: A71568  
 R:Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, Science 282, 754-759, 1998  
 A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis  
 A:Reference number: A71570; MUID:99000809  
 A:Accession: A71568  
 A:Molecule type: DNA  
 A:Status: preliminary  
 A:Residues: 1-242 <ARN>  
 A:Cross-references: GB:AE001276; GB:AE001273; NID:g3328399; PIDN:AA67606.1; PID:g3328400  
 A:Experimental source: serotype D, strain UW-3/Cx  
 C:Genetics:  
 A:Gene: CT016

Query Match 10.3%; Score 75; DB 2; Length 242;  
 Best Local Similarity 25.0%; Pred. No. 2.1;  
 Matches 20; Conservative 7; Mismatches 21; Indels 32; Gaps 3;  
 QY 41 PEAYCLRCGLTGL-----FGEDVFRSAPVYMTVVLRRTPACAGRSVYT--- 88  
 Db 161 PEPHCNCLHCQIGRATVEEDAGVSDLTFRSWDI-----SQSGEKMYTVD 208  
 QY 89 -----EAYVTIPVGCCT 100  
 Db 209 PLNPEQFNVLGTPIGCTC 228

RESULT 11  
 S22395  
 fetuin precursor - pig (fragment)  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 07-Apr-1994 #sequence\_revision 07-Apr-1994 #text\_change 21-Jul-2000  
 C:Accession: S22395; S22142  
 R:Brown, W.M.; Dziegielewska, K.M.; Saunders, N.R.; Christie, D.L.; Nawratil, P.; Muelle Eur. J. Biochem. 205, 321-331, 1992  
 A:Title: The nucleotide and deduced amino acid structures of sheep and pig fetuin. Commu  
 A:Reference number: S22394; MUID:92209519  
 A:Accession: S22395  
 A:Molecule type: mRNA  
 A:Residues: 1-362 <BRW>  
 A:Cross-references: EMBL:X56021; NID:g2104; PIDN:CAA39498.1; PID:g3980229  
 C:Superfamily: alpha-2-HS-glycoprotein; cystatin homology  
 C:Keywords: calcium binding; EF hand; glycoprotein  
 F:1-15/Domain: signal sequence (fragment) #status predicted <SIG>  
 F:16-362/Product: fetuin #status predicted <MAT>  
 F:20-134/Domain: cystatin homology <CY1>  
 F:143-249/Domain: cystatin homology <CY2>  
 F:96,153,173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.3%; Score 75; DB 2; Length 362;  
 Best Local Similarity 27.6%; Pred. No. 3.3;  
 Matches 27; Conservative 11; Mismatches 42; Indels 18; Gaps 3;  
 QY 30 SYDPARYPRYLPEAYCLRCGLTGLFGEDVFRSAPVYMTVVLRRTPACAGRSVYTE 89  
 Db 210 AYSPKCNLLVEKQYGFCKGTAKVNEEDVATCTVFTQPVLPQFAGA----- 261  
 QY 90 AYVTIPVGCCTVPEPEKADSNSSI-DKQAKLLG 126  
 Db 262 ----DAGAT----PVVDAANTASPLADYPAASLVVGP 290

RESULT 12  
 S28941  
 coagulation factor XIIa (EC 3.4.21.38) - guinea pig (fragment)  
 N:Alternate names: Hageman factor  
 C:Species: Cavia porcellus (guinea pig)

C>Date: 25-Feb-1994 #sequence\_revision 03-Aug-1995 #text\_change 21-Jan-2000  
 C:Accession: S28941  
 R:Samba, U.; Yamamoto, T.; Kunisada, T.; Shibuya, Y.; Tanase, S.; Kambara, T.; Okabe, Biochim. Biophys. Acta 1159, 113-121, 1992  
 A:Title: Primary structure of guinea-pig Hageman factor: sequence around the cleavage  
 A:Reference number: S28941; MUID:93003367  
 A:Accession: S28941  
 A:Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-603 <SEM>  
 A:Cross-references: EMBL:X68615; NID:g49578; PIDN:CAA48600.1; PID:g49579  
 C:Superfamily: coagulation factor XII; EGF homology; fibronectin type I repeat homolo  
 C:Keywords: hydrolase; serine proteinase  
 F:46-87/Domain: fibronectin type II repeat homology <1F2>  
 F:134-169/Domain: fibronectin type I repeat homology <1F2>  
 F:177-208/Domain: EGF homology <EGF>  
 F:216-294/Domain: kringle homology <KRG>  
 F:359-597/Domain: trypsin homology <TRY>

Query Match 10.3%; Score 75; DB 2; Length 603;  
 Best Local Similarity 22.2%; Pred. No. 5.7;  
 Matches 37; Conservative 17; Mismatches 59; Indels 54; Gaps 7;  
 QY 2 CPAGGRPADRRFRPPT-NLRSVSPWAYRISYDIPARYPRY-----LPEAY 44  
 Db 60 CIHKRGPGRPMCATTPNFDQDQWAYCL--EPKVKDHCXKHNPCORGICVNTLSSPH 117  
 QY 45 CLCRGCLTG-----LFGEDVFRSAPV-----YMTVVL 74  
 Db 118 CLCPDLHTGKHCQREKCFEPQLHRFFHENEIWFRTGPAVAKCHCKGPDHAKCHQMSQEC 177  
 QY 75 RRTPCACAGRSVYTEAY--VTIPVGCCTVPEPEKADSNSSIDKOG 119  
 Db 178 QTNPCNLNGRCLVEGHHLCDCPMGYT---GPFCDLDTTASCVEGRG 221

RESULT 13  
 T38292  
 hypothetical protein SPAC23E2.02 - fission yeast (Schizosaccharomyces pombe)  
 C:Species: Schizosaccharomyces pombe  
 C>Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 03-Dec-1999  
 C:Accession: T38292  
 R:Skelton, J.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V. submitted to the EMBL Data Library, January 1996  
 A:Reference number: Z21784  
 A:Accession: T38292  
 A:Status: preliminary; translated from GB/EMBL/DDBJ  
 A:Molecule type: DNA  
 A:Residues: 1-1273 <SKE>  
 A:Cross-references: EMBL:Z68887; PIDN:CAA93114.1; GSPDB:GN00066; SPDB:SPAC23E2.02  
 A:Experimental source: strain 972h-; cosmid G23E2  
 C:Genetics:  
 A:Gene: SPDB:SPAC23E2.02  
 A:Map position: 1  
 A:Introns: 8/2; 862/3

Query Match 10.2%; Score 74.5; DB 2; Length 1273;  
 Best Local Similarity 25.6%; Pred. No. 15;  
 Matches 22; Conservative 15; Mismatches 48; Indels 1; Gaps 1;  
 QY 46 LCRGCLTGLFGEDVFRSAPVYMTVVLRRTPACAGRSVYTEAYVTIPVGCCTVPEPE 105  
 Db 520 ICARQLTGLFSQVSSSFLSKNELPPKVIILEAKERTGGR-IYSRALPVSHTSATINHHT 578  
 QY 106 KDADSINSSIDKQGAALLGPNDA 131  
 Db 579 SNSNSISSNSTSLNPKDVTDPDPSHPS 604

RESULT 14  
 A55535

C:Accession: B81719  
R:Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey,  
C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,  
Nucleic Acids Res. 28, 1397-1406, 2000  
A:Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.  
A:Reference number: A81500; MUID:20150255  
A:Accession: B81719  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-242 <FT>  
A:Cross-references: GB:AE002296; GB:AE002160; NID:g7190325; PIDN:AAF39152.1; PID:g719032  
A:Experimental source: strain Nigg (MoPn)  
C:Genetics:  
A:Gene: TC0284

Query Match 10.4%; Score 76; DB 2; Length 242;  
Best Local Similarity 26.2%; Pred. No. 1.7;  
Matches 21; Conservative 6; Mismatches 21; Indels 32; Gaps 3;  
Qy 41 PEAVCLRCGLTGLF-----GEEDVRSAPVYPTVLLRTPACAGGRSVYt--- 88  
Db 161 PEPHCNLCUQIGRIAEEDIEVSEEDLFRSWDI-----SQYGEKMYTVD 208  
Qy 89 -----EAYVTIPVGCTC 100  
Db 209 PLNPEEQFNVLGTPIGCTC 228

RESULT 7  
A84663  
probable beta-ketoacyl-CoA synthase [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Feb-2001 #sequence\_revision 02-Feb-2001 #text\_change 02-Feb-2001  
C:Accession: A84663  
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;  
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.;  
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.  
Nature 402, 761-768, 1999  
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.  
A:Reference number: A84420; MUID:20083487  
A:Accession: A84663  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-509 <SPO>  
A:Cross-references: GB:AE002093; NID:g2760830; PIDN:AAB95298.1; GSPDB:GN00139  
C:Genetics:  
A:Map position: 2

Query Match 10.4%; Score 75.5; DB 2; Length 509;  
Best Local Similarity 31.3%; Pred. No. 4.2;  
Matches 26; Conservative 16; Mismatches 28; Indels 13; Gaps 5;  
Qy 48 RGCITGLFGEDVFRSAPVYPTVLLRTPACAGGRSVY-TEAYVTIPVGCTCVPEPEK 106  
Db 124 RSKLTGSFTEENLEFQR-----ILQRSGL---GESTYLPFAVLNVPPN-PCMKEARK 172  
Qy 107 DADSTN-SSIDKQAKLLLGPN 128  
Db 173 EAETVMFGAIDELLAKTNVNP 195

RESULT 8  
T44254  
thiamin biosynthesis protein thic [imported] - Rhizobium etli plasmid b  
C:Species: Rhizobium etli  
C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 21-Jul-2000  
C:Accession: T44254  
R:Miranda-Rios, J.; Morera, C.; Taboada, H.; Davalos, A.; Encarnacion, S.; Mora, J.; Sob  
J. Bacteriol. 179, 6887-6893, 1997  
A:Title: Expression of thiamin biosynthetic genes (thiCOG) and production of symbiotic

A:Reference number: Z22737; MUID:98037482  
A:Accession: T44254  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-610 <MIR>  
A:Cross-references: EMBL:AF004408; NID:g2627325; PIDN:AAG45972.1; PID:g2627326  
A:Experimental source: strain CE3  
C:Genetics:  
A:Gene: thic  
A:Genome: plasmid b  
C:Function:  
A:Description: involved in the biosynthesis of the pyrimidine moiety of thiamin  
C:Superfamily: thiamin biosynthesis protein thic

Query Match 10.4%; Score 75.5; DB 2; Length 610;  
Best Local Similarity 29.9%; Pred. No. 5.1;  
Matches 38; Conservative 14; Mismatches 54; Indels 21; Gaps 7;  
Qy 3 PAGGRPADRRFRPTNLRVSYPW---AVRISYDPARYPRYLPEAYCLRCGLTGLFGE-- 57  
Db 44 PTSGEp-----PVTVDSSGPTYDPAHVISID-AGLPR-LRESWIKARGDVESYDGRIV 95  
Qy 58 --EDVRSAPVYPTVLLRTPACA--GGRSVYTEAYVTIPVGCTCVPEPEKDAIDSINS 114  
Db 96 KPEDNGFATGERTPEPPVRNTPLKAKAGRAVTLAYAR-----AGIVTPEMEFIAIREN 150  
Qy 115 IDKQAK 121  
Db 151 LGRQAK 157

RESULT 9  
D72281  
hypothetical protein TM1214 - Thermotoga maritima (strain MSB8)  
C:Species: Thermotoga maritima  
C:Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000  
C:Accession: D72281  
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hic  
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson,  
C.M.  
Nature 399, 323-329, 1999  
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome  
A:Reference number: A72200; MUID:99287316  
A:Accession: D72281  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-178 <ARN>  
A:Cross-references: GB:AE001778; GB:AE000512; NID:g4981757; PIDN:AAD36289.1; PID:g498  
A:Experimental source: strain MSB8  
C:Genetics:  
A:Gene: TM1214  
C:Superfamily: psbG protein

Query Match 10.3%; Score 75; DB 2; Length 178;  
Best Local Similarity 23.1%; Pred. No. 1.5;  
Matches 34; Conservative 12; Mismatches 35; Indels 56; Gaps 7;  
Qy 18 NLRVSPPWAYRISYDPARYPRYLPEAYCLRCG-----LTGLFGEDVFRFSAPV-- 67  
Db 13 NLRSRISWMLH-----YCTCGGAVELPPSMTSRFDME--RFGIAPMAT 53  
Qy 68 -----YMPVTVLRRT-----PACAGGRSVYTEAVT----- 93  
Db 54 PRQADILLITGLYTKTLRRVITYTEOMPDPKYVVGFGSGCTINGIYFDSATVNRLDYY 113  
Qy 94 IPVG---CTCVPPEKDAIDSINSIDK 117  
Db 114 IPVDVIAGCMFRAEILAEAFNYLMEK 140  
RESULT 10

A;Gene: 13  
C;Superfamily: saimiri herpesvirus immediate-early protein 2  
C;Keywords: early protein

Qy	20	RSVSPWAIYRISDPA RYLPYLDEAYCICRG C--LTGLFGEEDVRFRSAPVMPTVLRR	77
Db	52	RALCPDDRVNVOESRG PKLIAEVCILCKKSGSTGAF----- CMPIVRKVPLRRV	103

**QY**      78 PAC--AGGRSVTEAYVTIPVGC-TCVPEPXA 108  
              :  
              :  
              :

**Dd**     104 -SCDRSTGLNNYVRSTELITVGCHSVLPRTORAA 136

RESULT 5

T2/843  
hypothetical protein ZK39.8 - Caenorhabditis ele

```

RESULT      5
T27843
hypothetical protein ZK39.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27843
R:Kershaw, J.
submitted to the EMBL Data Library, November 1996
A:Reference number: Z20428
A:Accession: T27843
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-226 <WIL>
A:CROSS-references: EMBL:Z82093; PIDN:CAB05021.1; GSPDB:GN00019; CESP:ZK39.8
A:Experimental source: clone ZK39
C:Genetics:
A:Gene: CESP:ZK39.8
A:Map position: 1
A:Introns: 32/1; 52/3; 108/1

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Query Match	10.8%	Score 78.5;	DB 2;	Length 226;
Best Local Similarity	25.4%	Pred. NO. 0.85;		
Matches	31;	Conservative	18;	Mismatches 32;
Indels	41;	Gaps	8;	

[illegible]

QY  
TTT  
NS  
TTT

Db I44 NS I45

RESULT 6  
B81719 conserved hypothetical protein TC0284 [imported] - Chlamydia muridarum (strain C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn C;date: 31-Mar-2000 #sequence revision 31-Mar-2000 #text change 11-May-2000





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RESULT      12
US-60-309-936-2
; Sequence 2, Application US/60309936
; GENERAL INFORMATION:
; APPLICANT: Llu, Ling
; APPLICANT: retreault Jonathan
; TITLE OF INVENTION: Methods of Using A Human IL-17 Related Polypeptide To Treat Disease
; FILE REFERENCE: P-14089A
; CURRENT APPLICATION NUMBER: US/60/309,936
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo sapiens
US-60-309-936-2

Query Match          25.7%; Score 187.5; DB 6; Length 197;
Best Local Similarity 40.2%; Pred. No. 2.6e-11;
Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

QY    17  TNLRSVSPNWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDVRFRFSADPYMPTVVLR 76
       : ::|||:: |:: |:: ||:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |:: |::
Db     101 THQRSISPWRYRVDTDDETRYPQKLFAECLCRCIDARTGRETAAALNSVRLQLSLVLR 160

QY    77  TPACAGGRSVYTEA-----YVTIPVGCTCV 101
       | _ | _ | _ | _ | _ | _ | _ | _ | _ | _ | _ | _ | _ | _ | _ | _ |
Db     161 RPSCRDGSGLTPGAFATFEETHVPVGCTCV 192

```

```

RESULT 14
US-09-854-280-12
; Sequence 12, Application US/09854280
; GENERAL INFORMATION:
; APPLICANT: Chen, Jian
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Goddard, Audrey
; APPLICANT: Gurney, Austin
; APPLICANT: Li, Hanzhong
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381RIC2
; CURRENT APPLICATION NUMBER: US/09/854,280
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: US 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: US 60/113,621
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 12
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: IL17B-FC fusion
US-09-854-280-12

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; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 4
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-908-827-4

Query Match      25.7%   Score 187.5; DB 5;   Length 197;
Best Local Similarity 40.2%; Pred. No. 2.6e-11;
Matches 37; Conservative 11; Mismatches 37; Indels 7; Gaps 1;

QY 17 TNLRSVPWAYRISYDPARYRPLPEAYCLRCGLTGLFGEEDVFRSAPVYMPVTLVR 76
    I: ||||| I: | ||| | ||||| I: | | : ||||
Db 101 THORSISPRWRYVDTHPKLAFACLCRCGIDARTGRTAALNSVRLQLSLVLR 160

QY 77 TPACAGGRSVYTEA-----VVTIPVGCTCV 101
    I: | | | | | : |||||
Db 161 RPCSRDGSGLTPGAFATFTEFIHVPGCTCV 192

RESULT 11
US-09-931-836-11
; Sequence 11, Application US/09931836
; GENERAL INFORMATION:
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3030R1C1
; CURRENT APPLICATION NUMBER: US/09/931,836
; PRIOR FILING DATE: 2001-08-16
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/112514
; PRIOR FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/113300
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/113430
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113605
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/113621

; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/114140
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/115552
; PRIOR FILING DATE: 1999-01-12
; PRIOR APPLICATION NUMBER: 60/116843
; PRIOR FILING DATE: 1999-01-22
; PRIOR APPLICATION NUMBER: 60/125774
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125778
; PRIOR FILING DATE: 1999-03-23
; PRIOR APPLICATION NUMBER: 60/125826
; PRIOR FILING DATE: 1999-03-24
; PRIOR APPLICATION NUMBER: 60/127035
; PRIOR FILING DATE: 1999-03-31
; PRIOR APPLICATION NUMBER: 60/127706
; PRIOR FILING DATE: 1999-04-05
; PRIOR APPLICATION NUMBER: 60/129122
; PRIOR FILING DATE: 1999-04-13
; PRIOR APPLICATION NUMBER: 60/130359
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131270
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131272
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/131291
; PRIOR FILING DATE: 1999-04-27
; PRIOR APPLICATION NUMBER: 60/132371
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132379
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/132383
; PRIOR FILING DATE: 1999-05-04
; PRIOR APPLICATION NUMBER: 60/135750
; PRIOR FILING DATE: 1999-05-25
; PRIOR APPLICATION NUMBER: 60/138166
; PRIOR FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: 60/144791
; PRIOR FILING DATE: 1999-07-20
; PRIOR APPLICATION NUMBER: 60/146970
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/162506
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: 09/311832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/874503
; PRIOR FILING DATE: 2001-06-05
; PRIOR APPLICATION NUMBER: 09/869599
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 09/908,827
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/28551
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: PCT/US99/30720
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
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; APPLICANT: Li, Hanzhong
; APPLICANT: Hillan, Kenneth
; APPLICANT: Tumas, Daniel
; APPLICANT: VanLookeren, Menno
; APPLICANT: Vandlen, Richard
; APPLICANT: Watanabe, Colin
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William
; APPLICANT: Yansura, Daniel
; TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
; FILE REFERENCE: P1381R1C1P1C1(US)
; CURRENT APPLICATION NUMBER: US/09/908,827
; CURRENT FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: 60/085,579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/113,621
; PRIOR FILING DATE: 1998-12-23
; PRIOR APPLICATION NUMBER: 60/130,232
; PRIOR FILING DATE: 1999-04-21
; PRIOR APPLICATION NUMBER: 60/131,022
; PRIOR FILING DATE: 1999-04-26
; PRIOR APPLICATION NUMBER: 60/134,287
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 60/138,387
; PRIOR FILING DATE: 1999-06-09
; PRIOR APPLICATION NUMBER: 60/172,096
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/175,481
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: 60/191,007
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/213,807
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/242,837
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: 60/244,072
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 09/311,832
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/380,138
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/380,142
; PRIOR FILING DATE: 1999-08-25
; PRIOR APPLICATION NUMBER: 09/644,848
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 09/747,259
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: PCT/US99/05028
; PRIOR FILING DATE: 1999-03-08
; PRIOR APPLICATION NUMBER: PCT/US99/10733
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/US99/31274
; PRIOR FILING DATE: 1999-12-30
; PRIOR APPLICATION NUMBER: PCT/US00/04341
; PRIOR FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/US00/05601
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: 2000-03-02
; PRIOR APPLICATION NUMBER: PCT/US00/07532
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: PCT/US00/15264
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: PCT/US00/23328
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; PRIOR APPLICATION NUMBER: PCT/US00/30873
; PRIOR FILING DATE: 2000-11-10
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; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: PCT/US00/34956
; PRIOR FILING DATE: 2000-12-20
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 39
; SEQ ID NO 8
; LENGTH: 202
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-908-827-8

Query Match *99.5%; Score 725; DB 5; Length 202;
Best Local Similarity 99.2%; Pred. No. 7.8e-65;
Matches 132; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRFRPPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 SCPAGGRPGDRFRPPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 129
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 RFRSAPVYMPVTVLRRTACAGRSVYTYAYVTIPVGCTCVPEPEKADSSINSSIDKQGA 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 RFRSAPVYMPVTVLRRTACAGRSVYTYAYVTIPVGCTCVPEPEKADSSINSSIDKQGA 189
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 KLLGPNADAPAGP 133
   ||||| ||||| |||||
Db 190 KLLGPNADAPAGP 202
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 3
US-09-480-297A-6
; Sequence 6, Application US/09480297A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
; TITLE OF INVENTION: PURIFIED MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX0917K
; CURRENT APPLICATION NUMBER: US/09/480,297A
; CURRENT FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: 60/115,506
; PRIOR FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-480-297A-6

Query Match 84.1%; Score 613; DB 5; Length 151;
Best Local Similarity 99.1%; Pred. No. 8.1e-54;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRFRPPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40 SCPAGGRPADRRFRPPTNLRSPWAYRISYDPAARYPRYLPEAYCLRCGLTGLFGEEDV 99
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 RFRSAPVYMPVTVLRRTACAGRSVYTYAYVTIPVGCTCVPEPEKADSSIN 112
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 100 RFRSAPVYMPVTVLRRTACAGRSVYTYAYVTIPVGCTCVPEPEKADSSIN 151
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-09-480-297A-12
; Sequence 12, Application US/09480297A
; GENERAL INFORMATION:
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Kastelein, Robert A.
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 5, 2001, 15:19:50 ; Search time 16.65 Seconds  
(without alignments)  
377.498 Million cell updates/sec

**Title:** US-09-320-713-4\_COPY\_28\_160

Perfect score: 729  
Sequence: 1 SCPACGRPADRRPRPPTNLR.....SIDQGAKLLLGNDAPAGP 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 309837 seqs, 47258215 residues

Total number of hits satisfying chosen parameters: 309837

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Pending\_Patents\_AA\_New:\*

1: /cgn2\_6/ptodata/2/paa/PCT\_NEW\_COMB.pcp.\*  
2: /cgn2\_6/ptodata/2/paa/US06\_NEW\_COMB.pcp.\*  
3: /cgn2\_6/ptodata/2/paa/US07\_NEW\_COMB.pcp.\*  
4: /cgn2\_6/ptodata/2/paa/US08\_NEW\_COMB.pcp.\*  
5: /cgn2\_6/ptodata/2/paa/US09\_NEW\_COMB.pcp.\*  
6: /cgn2\_6/ptodata/2/paa/US00\_NEW\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	729	100.0	202	5	US-09-480-297A-8	Sequence 8, Appli
2	725	99.5	202	5	US-09-908-827-8	Sequence 8, Appli
3	613	84.1	151	5	US-09-480-297A-6	Sequence 6, Appli
4	601	82.4	205	5	US-09-480-297A-10	Sequence 12, Appli
5	208	28.5	44	5	US-09-480-297A-12	Sequence 10, Appli
6	193	26.5	425	5	US-09-854-280-13	Sequence 13, Appli
7	187.5	25.7	197	5	US-09-886-404-8	Sequence 8, Appli
8	187.5	25.7	197	5	US-09-480-297A-23	Sequence 23, Appli
9	187.5	25.7	197	5	US-09-854-280-3	Sequence 3, Appli
10	187.5	25.7	197	5	US-09-908-827-4	Sequence 4, Appli
11	187.5	25.7	197	5	US-09-931-836-11	Sequence 11, Appli
12	187.5	25.7	197	6	US-60-309-936-2	Sequence 2, Appli
13	187.5	25.7	206	5	US-09-854-280-24	Sequence 24, Appli
14	176.5	24.2	408	5	US-09-854-280-12	Sequence 12, Appli
15	174	23.9	117	5	US-09-886-404-7	Sequence 7, Appli
16	174	23.9	175	5	US-09-854-280-23	Sequence 23, Appli
17	174	23.9	180	5	US-09-480-297A-2	Sequence 2, Appli
18	174	23.9	180	5	US-09-854-280-1	Sequence 1, Appli
19	174	23.9	180	5	US-09-908-827-2	Sequence 2, Appli
20	174	23.9	180	5	US-09-929-404-150	Sequence 150, App
21	173	23.7	180	5	US-09-480-297A-4	Sequence 4, Appli
22	169	23.2	117	5	US-09-886-404-6	Sequence 6, Appli
23	155.5	21.3	163	5	US-09-908-827-10	Sequence 10, Appli
24	139.5	19.1	123	5	US-09-480-297A-21	Sequence 21, Appli
25	130.5	17.9	155	5	US-09-886-404-5	Sequence 5, Appli
26	130.5	17.9	155	5	US-09-480-297A-33	Sequence 33, Appli
27	130.5	17.9	155	5	US-09-854-280-11	Sequence 11, Appli



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; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-817-4

Query Match          100.0%; Score 729; DB 15; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 54 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 113
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 114 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 173
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 KLLGPNDAAPG 133
Db 174 KLLGPNDAAPG 186

RESULT 13
US-09-397-846-4
; Sequence 4, Application US/09397846
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846
; CURRENT FILING DATE: 1999-09-17
; EARLIER APPLICATION NUMBER: 60/100,706
; EARLIER FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-846-4

Query Match          100.0%; Score 729; DB 17; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 54 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 113
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 114 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 173
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 KLLGPNDAAPG 133
Db 174 KLLGPNDAAPG 186

RESULT 14
US-09-397-846B-4
; Sequence 4, Application US/09397846B
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; APPLICANT: Foley, Kevin P.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846B
; CURRENT FILING DATE: 2001-05-21
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; PRIOR APPLICATION NUMBER: 60/100,706
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-846B-4

Query Match          100.0%; Score 729; DB 17; Length 186;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 54 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 113
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 114 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 173
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 KLLGPNDAAPG 133
Db 174 KLLGPNDAAPG 186

RESULT 15
US-09-154-817-3
; Sequence 3, Application US/09154817
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott
; APPLICANT: Taft, David
; APPLICANT: Foley, Kevin
; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54X
; CURRENT APPLICATION NUMBER: US/09/154,817
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 187
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-817-3

Query Match          100.0%; Score 729; DB 15; Length 187;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 60
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 55 SCAGGPPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEDV 114
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 115 RFRSAPVYMTVVLRRTPACAGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 174
   ||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 KLLGPNDAAPG 133
Db 175 KLLGPNDAAPG 187

Search completed: October 5, 2001, 15:22:57
Job time: 187 sec
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Query Match      100.0%; Score 729; DB 21; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 41 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 100
QY 61 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 101 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 160
QY 121 KLLGPNADAPAGP 133
Db 161 KLLGPNADAPAGP 173

RESULT 9
US-09-154-817-5
; Sequence 5, Application US/09154817
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott
; APPLICANT: Taft, David
; APPLICANT: Foley, Kevin
; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54X
; CURRENT APPLICATION NUMBER: US/09/154,817
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-154-817-5
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Query Match      100.0%; Score 729; DB 15; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 53 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 112
QY 61 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 113 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 172
QY 121 KLLGPNADAPAGP 133
Db 173 KLLGPNADAPAGP 185

RESULT 10
US-09-397-846-5
; Sequence 5, Application US/09397846
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; APPLICANT: Foley, Kevin P.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846
; CURRENT FILING DATE: 1999-09-17
; EARLIER APPLICATION NUMBER: 60/100,706
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-09-397-846-5

Query Match      100.0%; Score 729; DB 17; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 53 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 112
QY 61 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 113 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 172
QY 121 KLLGPNADAPAGP 133
Db 173 KLLGPNADAPAGP 185

RESULT 11
US-09-397-846B-5
; Sequence 5, Application US/09397846B
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Taft, David W.
; APPLICANT: Foley, Kevin P.
; TITLE OF INVENTION: Mammalian Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54
; CURRENT APPLICATION NUMBER: US/09/397,846B
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/100,706
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 185
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-397-846B-5

Query Match      100.0%; Score 729; DB 17; Length 185;
Best Local Similarity 100.0%; Pred. No. 1.7e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
Db 53 SCPAGRPADRRFRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 112
QY 61 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 120
Db 113 RFRSAPVYMTVVLRRTTPACAGRSVYTEAYVTIPVGCTCVPEPEKDADSINSSIDKQGA 172
QY 121 KLLGPNADAPAGP 133
Db 173 KLLGPNADAPAGP 185

RESULT 12
US-09-154-817-4
; Sequence 4, Application US/09154817
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott
; APPLICANT: Taft, David
; APPLICANT: Foley, Kevin
; TITLE OF INVENTION: Transforming Growth Factor Beta - 9
; FILE REFERENCE: 98-54X
; CURRENT APPLICATION NUMBER: US/09/154,817
; CURRENT FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
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; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-731-816-4

Query Match          100.0%; Score 729; DB 21; Length 160;
Best Local Similarity 100.0%; Pred. No. 1.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGPADRRFPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 60
   |||||||
Db 28 SCPAGGPADRRFPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 87
   |||||||

QY 61 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   |||||||
Db 88 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 147
   |||||||

QY 121 KLLGPNADAPAGP 133
   |||||||
Db 148 KLLGPNADAPAGP 160
   |||||||

RESULT 6
PCT-US99-11644-32
; Sequence 32, Application PC/TUS9911644
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470PCT
; CURRENT APPLICATION NUMBER: PCT/US99/11644
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-11644-32

Query Match          100.0%; Score 729; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGPADRRFPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 60
   |||||||
Db 41 SCPAGGPADRRFPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 100
   |||||||

QY 61 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   |||||||
Db 101 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 160
   |||||||

QY 121 KLLGPNADAPAGP 133
   |||||||
Db 161 KLLGPNADAPAGP 173
   |||||||
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```
RESULT 7
US-09-320-713-32
; Sequence 32, Application US/09320713
; GENERAL INFORMATION:
; APPLICANT: Reinhard Ebner
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470
; CURRENT APPLICATION NUMBER: US/09/320,713
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 32
; LENGTH: 173
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-320-713-32

Query Match          100.0%; Score 729; DB 17; Length 173;
Best Local Similarity 100.0%; Pred. No. 1.5e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGPADRRFPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 60
   |||||||
Db 41 SCPAGGPADRRFPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGCLTGLFGEEDV 100
   |||||||

QY 61 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 120
   |||||||
Db 101 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTPVGCTCVPEPKDADSINSSIDKQGA 160
   |||||||

QY 121 KLLGPNADAPAGP 133
   |||||||
Db 161 KLLGPNADAPAGP 173
   |||||||

RESULT 8
US-09-731-816-32
; Sequence 32, Application US/09731816
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Ruben, Steven
; TITLE OF INVENTION: Interleukins-21 and 22
; FILE REFERENCE: PF470P1
; CURRENT APPLICATION NUMBER: US/09/731,816
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/169,837
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/320,713
; PRIOR FILING DATE: 1999-05-27
; PRIOR APPLICATION NUMBER: 60/087,340
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/099,805
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/131,965
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: PCT US99/11644
; PRIOR FILING DATE: 1999-05-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 32
; LENGTH: 173
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-731-816-32
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Db      148 KLLGPNDA PGP 160
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RESULT      2
PCT-US99-11644-4
; Sequence 4, Application PC/TUS9911644
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: INTERLEUKINS-21 AND 22
; FILE REFERENCE: PF470PCT
; CURRENT APPLICATION NUMBER: PCT/US99/11644
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: 60/087,340
; EARLIER FILING DATE: 1998-05-29
; EARLIER APPLICATION NUMBER: 60/099,805
; EARLIER FILING DATE: 1998-09-10
; EARLIER APPLICATION NUMBER: 60/131,965
; EARLIER FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US99-11644-4

Query Match      100.0%; Score 729; DB 1; Length 160;
Best Local Similarity      100.0%; Pred. No. 1.4e-73;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      1 SCPAGGRPADRRFRPPTNLRSLVSPWAYRISYDPA RYPLPEAYCLRCGLTGLFGEDV 60
      |||||||
Db      28 SCPAGGRPADRRFRPPTNLRSLVSPWAYRISYDPA RYPLPEAYCLRCGLTGLFGEDV 87
      |||||||

QY      61 RFRSAPVYMPVTWLRT PACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSI NSSIDKQGA 120
      |||||||
Db      88 RFRSAPVYMPVTWLRT PACAGGRSVYTEAYVTIPVGCTCVPEPEKDADSI NSSIDKQGA 147
      |||||||

QY      121 KLLGPNDA PGP 133
      |||||||
Db      148 KLLGPNDA PGP 160
|||||

RESULT      3
US-09-231-788-12
; Sequence 12, Application US/09231788A
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Interleukin-20
; FILE REFERENCE: PF399P1
; CURRENT APPLICATION NUMBER: US/09/231,788A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: 60/052,870
; EARLIER FILING DATE: 1997-07-16
; EARLIER APPLICATION NUMBER: 60/055,952
; EARLIER FILING DATE: 1997-08-18
; EARLIER APPLICATION NUMBER: 60/060,140
; EARLIER FILING DATE: 1997-09-26
; EARLIER APPLICATION NUMBER: 09/115,832
; EARLIER FILING DATE: 1998-07-15
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 160
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-231-788-12

Query Match      100.0%; Score 729; DB 16; Length 160;
Best Local Similarity      100.0%; Pred. No. 1.4e-73;

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Matches	133;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
QY	1	SCPAGGRPADRRFRPPTNLRISVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV	60						
DB	28	SCPAGGRPADRRFRPPTNLRISVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV	87						
QY	61	RFRSAPVYMTVVLLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKADDSINSSIDKQA	120						
DB	88	RFRSAPVYMTVVLLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKADDSINSSIDKQA	147						
QY	121	KLLIGPNDA PAGP	133						
DB	148	KLLIGPNDA PAGP	160						
RESULT	4								
US-09-320-713-4		; Sequence 4, Application US/09320713							
		; GENERAL INFORMATION:							
		; APPLICANT: Reinhard Ebner							
		; APPLICANT: Steven M. Ruben							
		; TITLE OF INVENTION: INTERLEUKINS-21 AND 22							
		; FILE REFERENCE: PF470							
		; CURRENT APPLICATION NUMBER: US/09/320,713							
		; CURRENT FILING DATE: 1999-05-27							
		; EARLIER APPLICATION NUMBER: 60/087,340							
		; EARLIER FILING DATE: 1998-05-29							
		; EARLIER APPLICATION NUMBER: 60/099,805							
		; EARLIER FILING DATE: 1998-09-10							
		; EARLIER APPLICATION NUMBER: 60/131,965							
		; EARLIER FILING DATE: 1999-04-30							
		; NUMBER OF SEQ ID NOS: 32							
		; SOFTWARE: PatentIn Ver. 2.0							
		; SEQ ID NO 4							
		; LENGTH: 160							
		; TYPE: PRT							
		; ORGANISM: Homo sapiens							
US-09-320-713-4									
Query Match		100.0%; Score 729; DB 17; Length 160;							
Best Local Similarity		100.0%; Pred. No. 1.4e-73;							
Matches	133;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0
QY	1	SCPAGGRPADRRFRPPTNLRISVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV	60						
DB	28	SCPAGGRPADRRFRPPTNLRISVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV	87						
QY	61	RFRSAPVYMTVVLLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKADDSINSSIDKQA	120						
DB	88	RFRSAPVYMTVVLLRRTACAGRSVYTEAYVTIPVGCTCVPEPEKADDSINSSIDKQA	147						
QY	121	KLLIGPNDA PAGP	133						
DB	148	KLLIGPNDA PAGP	160						
RESULT	5								
US-09-731-816-4		; Sequence 4, Application US/09731816							
		; GENERAL INFORMATION:							
		; APPLICANT: Ebner, Reinhard							
		; APPLICANT: Ruben, Steven							
		; TITLE OF INVENTION: Interleukins-21 and 22							
		; FILE REFERENCE: PF470P1							
		; CURRENT APPLICATION NUMBER: US/09/731,816							
		; CURRENT FILING DATE: 2000-12-08							
		; PRIOR APPLICATION NUMBER: 60/169,837							
		; PRIOR FILING DATE: 1999-12-09							
		; PRIOR APPLICATION NUMBER: 09/320,713							
		; PRIOR FILING DATE: 1999-05-27							
		; PRIOR APPLICATION NUMBER: 60/087,340							
		; PRIOR FILING DATE: 1998-05-29							

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(without alignments)  
337.749 Million cell updates/sec

Title: US-09-320-713-4\_COPY\_28\_160

Perfect score: 729

Sequence: 1 SCFAGGRRPDRRPPPTNLR.....SIDKQAKLLGPNDAPAGP 133

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2803329 seqs, 221847457 residues

Total number of hits satisfying chosen parameters: 2803329

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Pending\_Patents\_AA\_Main:\*

- 1: /cgn2\_6/ptodata/2/paa/PCTUS\_COMB.pcp.\*
- 2: /cgn2\_6/ptodata/2/paa/US06\_COMB.pcp.\*
- 3: /cgn2\_6/ptodata/2/paa/US07\_COMB.pcp.\*
- 4: /cgn2\_6/ptodata/2/paa/US080\_COMB.pcp.\*
- 5: /cgn2\_6/ptodata/2/paa/US081\_COMB.pcp.\*
- 6: /cgn2\_6/ptodata/2/paa/US082\_COMB.pcp.\*
- 7: /cgn2\_6/ptodata/2/paa/US083\_COMB.pcp.\*
- 8: /cgn2\_6/ptodata/2/paa/US084\_COMB.pcp.\*
- 9: /cgn2\_6/ptodata/2/paa/US085\_COMB.pcp.\*
- 10: /cgn2\_6/ptodata/2/paa/US086\_COMB.pcp.\*
- 11: /cgn2\_6/ptodata/2/paa/US087\_COMB.pcp.\*
- 12: /cgn2\_6/ptodata/2/paa/US088\_COMB.pcp.\*
- 13: /cgn2\_6/ptodata/2/paa/US089\_COMB.pcp.\*
- 14: /cgn2\_6/ptodata/2/paa/US090\_COMB.pcp.\*
- 15: /cgn2\_6/ptodata/2/paa/US091\_COMB.pcp.\*
- 16: /cgn2\_6/ptodata/2/paa/US092\_COMB.pcp.\*
- 17: /cgn2\_6/ptodata/2/paa/US093\_COMB.pcp.\*
- 18: /cgn2\_6/ptodata/2/paa/US094\_COMB.pcp.\*
- 19: /cgn2\_6/ptodata/2/paa/US095\_COMB.pcp.\*
- 20: /cgn2\_6/ptodata/2/paa/US096\_COMB.pcp.\*
- 21: /cgn2\_6/ptodata/2/paa/US097\_COMB.pcp.\*
- 22: /cgn2\_6/ptodata/2/paa/US098\_COMB.pcp.\*
- 23: /cgn2\_6/ptodata/2/paa/US060\_COMB.pcp.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729	100.0	160	1	PCT-US00-00807-12
2	729	100.0	160	1	PCT-US99-11644-4
3	729	100.0	160	16	US-09-231-788-12
4	729	100.0	160	17	US-09-320-713-4
5	729	100.0	160	21	US-09-731-816-4
6	729	100.0	173	1	PCT-US99-11644-32
7	729	100.0	173	1	US-09-320-713-32
8	729	100.0	173	21	US-09-731-816-32
9	729	100.0	185	15	US-09-154-817-5
10	729	100.0	185	17	US-09-397-846-5

11	729	100.0	185	17	US-09-397-846B-5	Sequence 5, Appli
12	729	100.0	186	15	US-09-154-817-4	Sequence 4, Appli
13	729	100.0	186	17	US-09-397-846-4	Sequence 4, Appli
14	729	100.0	186	17	US-09-397-846B-4	Sequence 4, Appli
15	729	100.0	187	15	US-09-154-817-3	Sequence 3, Appli
16	729	100.0	187	17	US-09-397-846-3	Sequence 3, Appli
17	729	100.0	187	17	US-09-397-846-18	Sequence 18, Appli
18	729	100.0	187	17	US-09-397-846B-3	Sequence 3, Appli
19	729	100.0	187	17	US-09-397-846B-18	Sequence 18, Appli
20	729	100.0	202	15	US-09-154-817-2	Sequence 2, Appli
21	729	100.0	202	17	US-09-397-846-2	Sequence 2, Appli
22	729	100.0	202	17	US-09-397-846B-2	Sequence 2, Appli
23	729	100.0	209	17	US-09-397-846-17	Sequence 17, Appli
24	729	100.0	209	17	US-09-397-846B-17	Sequence 17, Appli
25	725	99.5	202	21	US-09-747-259-8	Sequence 8, Appli
26	725	99.5	202	22	US-09-816-744-8	Sequence 8, Appli
27	601	82.4	183	17	US-09-397-846-12	Sequence 12, Appli
28	601	82.4	183	17	US-09-397-846B-12	Sequence 12, Appli
29	601	82.4	205	17	US-09-397-846-9	Sequence 9, Appli
30	601	82.4	205	17	US-09-397-846B-9	Sequence 9, Appli
31	601	82.4	205	21	US-09-724-864-37	Sequence 37, Appli
32	303	41.6	57	17	US-09-397-846-21	Sequence 21, Appli
33	303	41.6	57	17	US-09-397-846B-21	Sequence 21, Appli
34	242	33.2	54	17	US-09-397-846-19	Sequence 19, Appli
35	242	33.2	54	17	US-09-397-846B-19	Sequence 19, Appli
36	193	26.5	425	17	US-09-311-832-13	Sequence 13, Appli
37	187.5	25.7	179	16	US-09-283-810-3	Sequence 3, Appli
38	187.5	25.7	197	1	PCT-US99-11644-29	Sequence 29, Appli
39	187.5	25.7	197	16	US-09-283-810-2	Sequence 2, Appli
40	187.5	25.7	197	17	US-09-311-832-3	Sequence 3, Appli
41	187.5	25.7	197	17	US-09-320-713-29	Sequence 29, Appli
42	187.5	25.7	197	18	US-09-409-441-2	Sequence 2, Appli
43	187.5	25.7	197	21	US-09-731-816-29	Sequence 29, Appli
44	187.5	25.7	197	21	US-09-747-259-4	Sequence 4, Appli
45	187.5	25.7	197	23	US-60-266-159-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1  
PCT-US00-00807-12  
; Sequence 12, Application PC/TUS00000807  
; GENERAL INFORMATION:  
; APPLICANT: Human Genome Sciences, Inc.  
; TITLE OF INVENTION: Interleukin-20  
; FILE REFERENCE: PF399PCY2  
; CURRENT APPLICATION NUMBER: PCT/US00/00807  
; CURRENT FILING DATE: 2000-01-14  
; EARLIER APPLICATION NUMBER: 09/231,788  
; EARLIER FILING DATE: 1999-01-15  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 12  
; LENGTH: 160  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
PCT-US00-00807-12

Query Match 100.0%; Score 729; DB 1; Length 160;  
Best Local Similarity 100.0%; Pred. No. 1.4e-73;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SCFAGGRRPDRRPPPTNLR	SVSPWAYRISYDPA	RYRPLPEAYCLRCGLTGLFGEDV	60
DB	28	SCFAGGRRPDRRPPPTNLR	SVSPWAYRISYDPA	RYRPLPEAYCLRCGLTGLFGEDV	87
QY	61	RFRSAPYMTVVLRRTP	PACAGGRSVTEAYVTIP	VGCTCVPEPEKADSI	120
DB	88	RFRSAPYMTVVLRRTP	PACAGGRSVTEAYVTIP	VGCTCVPEPEKADSI	147
QY	121	KLGLPNDAPAGP			133

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; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 151 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Herpesvirus Saimiri
; STRAIN: ORF13
; US-09-022-696-8

```

```

Query Match      14.9%; Score 108.5; DB 3; Length 151;
Best Local Similarity 31.4%; Pred. No. 3.3e-05;
Matches 27; Conservative 11; Mismatches 37; Indels 11; Gaps 3;

QY  20 RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDVRFERSADPVYMPVTVVLRRTPA 79
    ||||| : |||| : ||| : ||: | | | | | : | | : | | :
Db   65 RSTSPWTLHRNEDQDRYPSVIWEAKCRYLGCVNA-DGNVDYHMNSVPIQQEILVVRK--- 120
    ||||| : |||| : ||| : ||: | | | | | : | | : | | :

QY  80 CAGGRSVYTEAY----VTIPVGCTCV 101
    | : : |||||
Db  121 ---GHQPCPNFRLKMLVTVGCTCV 143

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Search completed: October 5, 2001, 15:20:11  
Job time: 21 sec





STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating S  
SOFTWARE: Microsoft Word for Apple,  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/022,257  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620,694  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/410,535  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-B  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 158 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-022-257-7

	Query Match	15.4%	Score 112;	DB 4;	Length 158;
	Best Local Similarity	33.3%;	Pred. NO. 1.4e-05;		
	Matches 33; Conservative	14;	Mismatches 44;	Indels	8; Gaps
QY	5	GGRPADRRFRPPNLL-RVSPFWAYRISYDPA RPYRLPEAYCLRCGLTGLFGEDVRFR	63		
		:   :   :   :   :   :   :   :   :			
DB	58	GAKVSSR--RPSDYLNRSTFPWLHRRNDPRPYSVEIAEQCRHQRCVNA--EGKLDHHMN	114		
		:   :   :   :   :   :   :   :   :			
QY	64	SAPVYMTVVLRTP-ACAGGRSVYTEAYVTIPVGTCV	101		
		:   :   :   :   :   :   :   :   :			
DB	115	SVLTGDEILVLKKREPSCP---PTFRFEKMLGVGGTCV	150		
		:   :   :   :   :   :   :   :   :			

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RESULT 12
US-08-620-694A-8
; Sequence 8, Application US/08620694A
; Patent No. 5869286
; GENERAL INFORMATION:
; APPLICANT: Yao, zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: NO. 5869286el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/620,694A
FILING DATE: 21 MARCH 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/538,765
FILING DATE: 7 AUGUST 1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: USSN 08/410,535
FILING DATE: 23 MARCH 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia Anne
REGISTRATION NUMBER: 34,695
REFERENCE/DOCKET NUMBER: 2617-B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)587-0430
TELEFAX: (206)
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 151 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Herpesvirus Saimiri
STRAIN: ORF13
US-08-620-694A-8

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	Query Match	14.9%;	Score 108.5;	DB 2;	Length 151;
	Best Local Similarity	31.4%;	Pred.No.3.e-05;		
	Matches 27;	Conservative 11;	Mismatches 37;	Indels 11;	Gaps
QY	20	RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLGEEDVDFRSPAPVTMPVTVLVRTPA	79		
		.    :     :     :     :		:	:
D6	65	RSTSPWTLHRNEDQDRYSVINAEKRYILGCVNA-DGNVDYHMNSVP IQOETLVVRK---	120		
		:     :     :     :		:	:
QY	80	CAGGRSPTYTEAY----VTIPVGCTCV	101		
		: : : :		:	:
D6	121	---GHOPCPSNFLEKMLVTVGCTCV	143		
		: : : :		:	:

RESULT 13  
US-09-034-810-6  
; Sequence 6, Application US/09034810  
; Patent No. 6043344  
; GENERAL INFORMATION:  
; APPLICANT: Jacobs, Kenneth  
; APPLICANT: Kelleher, Kerry  
; APPLICANT: Carlin, McKeough  
; APPLICANT: Goldman, Samuel  
; APPLICANT: Pittman, Debra  
; APPLICANT: Mi, Sha  
; APPLICANT: Neben, Steven  
; APPLICANT: Giannotti, JoAnn  
; APPLICANT: Golden/Fleet, Margaret  
TITLE OF INVENTION: Human CTLA-8 and Uses of CTLA-8-Related Proteins  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genetics Institute, Inc.  
STREET: 87 Cambridgepark Drive  
CITY: Cambridge  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02140  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

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: Sequence 7, Application US/09022259
: Patent No. 6191104el
:
: GENERAL INFORMATION:
:
: APPLICANT: Yao, Zhengbin
: APPLICANT: Spriggs, Melanie
: APPLICANT: Fanslow, William
: TITLE OF INVENTION: No. 6191104el Receptor That Binds IL-17
: NUMBER OF SEQUENCES: 10

```

NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101

STATE: WA  
COUNTRY: USA  
ZIP: 98101

COUNTRY: USA  
ZTP: 98101

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

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;
; COMPUTER: Apple Power Macintosh
;
; OPERATING SYSTEM: Apple Operating System 7.5.5
;
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
;

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; SOFTWARE: MICROSOFT WORD 101
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/023

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; APPLICATION NUMBER: US/09/022;  
 ; FILING DATE:  
 ; CLASSIFICATION:

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/620 694

; APPLICATION NUMBER: 08/620,694  
 ; FILING DATE:  
 ; CLASSIFICATION:

```

; CLASSIFICATION:
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: USSN 08/41

```

APPLICATION NUMBER: USSN 08/41  
FILING DATE: 23 MARCH 1995  
CLASSIFICATION:

CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins Patricia Anne

NAME: PEIKINS, PATRICIA ANNE  
REGISTRATION NUMBER: 34,695  
REFERENCE/DOCKET NUMBER: 2617-

REFERENCE/DOCREF NUMBER: 2617-  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430

TELEPHONE: (206) 587-0430  
TELEFAX: (206)  
INFORMATION FOR SEQ ID NO: 7:

```

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 158 amino acids

```

```

; LENGTH: 100 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

US-09-022-259-7

1  
2  
3  
4  
5  
6  
7  
8  
9  
10

Query Match	15.4%	Score
Best Local Similarity	33.3%	Predicted

Best Local Similarity 33.3%, Fixed  
Matches 33; Conservative 14; M

QY 5 GGRPADRRFRPPTNL-RSVSPWAYRISY

Db 58 GAKVSSR--RPSDYLNRRSTSPWTLHRNE

Qy 64 SAPVYMP TVLRRTP-ACAGGRSVYTEA

Db 115 SVLIQQEILVLKREPECP--FTFRVE

## RESULT 11

RESOLUT II  
US-09-022-257-7  
: Sequence 7. Application US/09022257

Sequence 1, Application 03/03022257  
; Patent No. 6197525  
: GENERAL INFORMATION:

APPLICANT: Yao, Zhengbin

APPLICANT: Spriggs, Melanie

; AFFILIANT: SPRINGS, MICHIGAN  
 ; APPLICANT: Fanslow, William  
 ; TITLE OF INVENTION: No. 6197525e

```

; FILE OF INVENTION: NO. 015,320
;
; NUMBER OF SEQUENCES: 10
;
; CORRESPONDENCE ADDRESS:

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ADDRESSEE: Immunex Corporation

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; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-255-7

Query Match 15.4%; Score 112; DB 3; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDYRFR 63
Db 58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDPDYPSVIWEAQCRHRCVNA-EGKLDHNM 114

QY 64 SAPYMPVTVLLRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
Db 115 SVLIQIQLVLRKRESCP---FTFRVEKMLVGVGCTCV 150

RESULT 7
US-09-022-696-7
; Sequence 7, Application US/09022696
; Patent No. 6072037
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6072037el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,696
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/620,694
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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US-09-022-696-7

Query Match 15.4%; Score 112; DB 3; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDYRFR 63
Db 58 GAKVSSR--RPSDYLNRSTSPWTLHRNEDPDYPSVIWEAQCRHRCVNA-EGKLDHNM 114

QY 64 SAPYMPVTVLLRTP-ACAGGRSVYTEAYVTIPVGCTCV 101
Db 115 SVLIQIQLVLRKRESCP---FTFRVEKMLVGVGCTCV 150

RESULT 8
US-09-022-253-7
; Sequence 7, Application US/09022253
; Patent No. 6096305
; GENERAL INFORMATION:
; APPLICANT: Yao, Zhengbin
; APPLICANT: Spriggs, Melanie
; APPLICANT: Fanslow, William
; TITLE OF INVENTION: No. 6096305el Receptor That Binds IL-17
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Power Macintosh
; OPERATING SYSTEM: Apple Operating System 7.5.5
; SOFTWARE: Microsoft Word for Apple, Version 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,253
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/620,694
; FILING DATE: 21-MARCH-1996
; APPLICATION NUMBER: USSN 08/538,765
; FILING DATE: 7 AUGUST 1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/410,535
; FILING DATE: 23 MARCH 1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,695
; REFERENCE/DOCKET NUMBER: 2617-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 158 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-022-253-7

Query Match 15.4%; Score 112; DB 3; Length 158;
Best Local Similarity 33.3%; Pred. No. 1.4e-05;
Matches 33; Conservative 14; Mismatches 44; Indels 8; Gaps 5;

QY 5 GGRPADRRFPPTNL-RSVSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDYRFR 63

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Db      36 SCPPVGGGSKLIDIGIINENQVRSMRSNRSRSTSPNNYTVTWDPNRPSEVVQAQRNL 90
Qy      49 GCLTGLFGEDYRRFSAPVYPTVVLRRTFACAGGRSV-YTEAYVTIPVGCTCV 101
       || :||| :|| :||| :||| :||| :||| :||| :||| :|||
Db      96 GCINAQ-GKEDISMNSVFIQETLVRRKHQ---GCSVSFQLEKVLVTVGCTCV 145

RESULT 2
US-08-833-823-12
; Sequence 12, Application US/08833823
; Patent No. 5969093
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Kelleher, Kerry
; APPLICANT: Carlin, McKeough
; TITLE OF INVENTION: DNA SEQUENCES AND SECRETED PROTEINS
; TITLE OF INVENTION: ENCODED THEREBY
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc. -- Legal Affairs
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,823
; FILING DATE: 10-APR-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/514,014
; FILING DATE: 11-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI6000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 153 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-833-823-12

Query Match          21.3%; Score 155.5; DB 2; Length 153;
Best Local Similarity 36.0%; Pred. No. 1.2e-10;
Matches 41; Conservative 15; Mismatches 41; Indels 17; Gaps

Qy      1 SC---PAGEPAD-----RRFRPPTNL--RVSWPAWRIISVDPARYPRLPEAVCLCR 48
       || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      36 SCPPVGGGSKLIDIGIINENQVRSMRSNRSRSTSPNNYTVTWDPNRPSEVVQAQRNL 95
Qy      49 GCLTGLFGEDYRRFSAPVYPTVVLRRTFACAGGRSV-YTEAYVTIPVGCTCV 101
       || :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db      96 GCINAQ-GKEDISMNSVFIQETLVRRKHQ---GCSVSFQLEKVLVTVGCTCV 145

RESULT 3
US-09-034-810-2
; Sequence 2, Application US/09034810
; Patent No. 6043344
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth

```





FT		/note= "phosphorylation site"
FT	Modified-site	164..166
FT		/note= "N-glycosylation site"
FT	Modified-site	166..168
FT		/note= "calcium phosphorylation site"
XX		
PN	WO200042188-A2.	
XX		
XX	20-JUL-2000.	
XX		
XX	10-JAN-2000; 2000WO-US000006.	
PF		
XX	11-JAN-1999; 99US-0228822.	
PR		
XX	(SCHE ) SCHERING CORP.	
XX		
XX	Gorman DM, Bazan JF, Kastelein RA;	
PI		
XX	WPI; 2000-466130/40.	
DR	N-PSDB; AAA58985.	
DR		
XX		
PT	New isolated polynucleotide encoding a mammalian Interleukin-17 like	
PT	protein used to identify genes for homologous proteins -	
XX	Claim 11; Page 15-16; l1lpp; English.	
XX		
CC	The present sequence represents an interleukin-173 (IL-173) polypeptide.	
CC	The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a	
CC	member of a new group of interleukins, IL-170 polypeptides. The members	
CC	comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170	
CC	protein can be used to treat abnormal proliferation e.g. cancer	
CC	or degenerative conditions. Antibodies can be used in diagnostic	
CC	methods to detect over production of IL-170 protein in cells or body	
CC	fluids.	
XX		
SQ	Sequence 205 AA;	
	Query Match 82.43; Score 601; DB 21; Length 205;	
	Best Local Similarity 83.38; Pred. No. 4.5e-60;	
	Matches 110; Conservative 6; Mismatches 12; Indels 4; Gaps 1;	
Qy	1 SCPAGGRPADRRFRPPTNLRSSVWARYISYDPAHYPRYLPEAYCLCRGCLTGLFGEEDV 60	
Db	77 scpaggaaadrrfrpptnlrsrspwayrissydparylpeayclcrcltglygeedf 136	
Qy	61 RFRSAPVYMPVTLRRTPACAGGRSVYTEAVVTIPVGCTCVPEPKDADSNSSIDKOGA 120	
	:                   :                   :	
Db	137 rfrstpvfspavvirrtaacaggrsvyaehyitipvgctcvpepkdsadsansmd---- 192	
Qy	121 KLLGPNDPAPAG 132	
Db	193 killigpadrag 204	
	RESULT 15	
	AAB07691	
ID	AAB07691 standard; Protein: 205 AA.	
XX		
XX	AAB07691;	
XX		
DT	07-NOV-2000 (first entry)	
XX		
DE	A murine interleukin-173 polypeptide.	
XX		
KW	Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;	
KW	IL-174; IL-176; IL-177; cell proliferation; cancer; ss.	
XX		
OS	Mus sp.	
XX		
XX		
Key	Location/Qualifiers	
FT	Peptide 1..24	
FT		/note= "signal peptide"



PT New DNA sequence encoding a mammalian homolog of CTLA-8, designated  
PT Interleukin-171 (IL-171), useful for recombinant production of IL-171  
PT which can be used for treating conditions associated with abnormal  
PT physiology or development -  
XX  
PS Disclosure; Page 97; 111pp; English.  
XX  
CC The present sequence represents an interleukin (IL)-173 polypeptide.  
CC It is a mammalian homologue of the cytokine designated CTLA-8 (also  
CC referred to as IL-17). The specification also describes homologues  
CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA  
CC sequence encoding IL-171 is useful for identifying genes, mRNA and  
CC cDNA molecules which code for related or homologous proteins. The  
CC IL-171 protein, antibodies against IL-171, and compounds which have  
CC binding affinity to IL-171 are useful in treatment of conditions  
CC associated with abnormal physiology or development, including abnormal  
CC proliferation, e.g. cancerous conditions, or degenerative conditions.  
CC The IL-171 protein can be used in kits and assay methods for identifying  
CC compounds that selectively bind to IL-171.  
XX  
SQ Sequence 151 AA;

Query Match 84.1%; Score 613; DB 21; Length 151;  
Best Local Similarity 99.1%; Pred. No. 1.4e-61;  
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 SCPAGGRPADRRFRPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60  
Db 40 SCPAGGRPADRRFRPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 99  
QY 61 RFRSAPVYMTVVLRTTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDIN 112  
Db 100 RFRSAPVYMTVVLRTTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDIN 151

RESULT 13  
AAY70658  
ID AAY70658 standard; Protein; 183 AA.  
XX  
AC AAY70658;  
DT 18-JUL-2000 (first entry)  
XX  
DE Mature murine transforming growth factor beta-9, Ztfgbeta-9 protein.  
XX  
KW Murine transforming growth factor beta-9; Ztfg beta-9;  
KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;  
KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;  
KW peripheral neuropathy; demyelinating disease; multiple sclerosis;  
KW antiviral; cytostatic.  
XX  
OS Mus sp.  
XX  
PN WO200015798-A2.  
XX  
PD 23-MAR-2000.  
XX  
PF 17-SEP-1999; 99WO-US21677.  
XX  
PR 17-SEP-1998; 98US-O154817.  
XX  
PA (ZYMO ) ZYMOGENETICS INC.  
XX  
PI Presnell SR, Taft DW, Foley KP;  
XX  
DR WPI: 2000-271436/23.  
DR N-PSDB; AA252198.  
XX  
XX Polynucleotides encoding a novel transforming growth factor beta-9  
PT polypeptide, designated ztfg beta-9, useful as an antiviral and  
PT antiproliferative agent -  
XX

PS Claim 6; Page 89; 97pp; English.  
XX  
CC The present sequence is the mature murine transforming growth factor  
CC beta-9, designated ztfg beta-9. The signal sequence extends from  
CC amino acid residues 1 to 22. Murine ztfg beta-9 was found to be highly  
CC expressed in the HCL hypothalamic cell line. This can be used  
CC to treat a variety of neurodegenerative diseases such as amyotrophic  
CC lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease,  
CC Parkinson's disease and peripheral neuropathies, or demyelinating  
CC diseases including multiple sclerosis. Ztfg beta-9 peptides have  
CC antiviral activity and may also be used to regulate the proliferation,  
CC differentiation and apoptosis of neurons, glial cells, lymphocytes,  
CC hematopoietic cells and stromal cells.  
XX  
SQ Sequence 183 AA;

Query Match 82.4%; Score 601; DB 21; Length 183;  
Best Local Similarity 83.3%; Pred. No. 3.9e-60;  
Matches 110; Conservative 6; Mismatches 12; Indels 4; Gaps 1;  
QY 1 SCPAGGRPADRRFRPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60  
Db 55 SCPAGGRPADRRFRPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 114  
QY 61 RFRSAPVYMTVVLRTTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDINSSIDKQGA 120  
Db 115 RFRSAPVYMTVVLRTTPACAGRSVYTAAYVTIPVGCCTVPEPEKADSDINSSIDKQGA 170  
QY 121 KLLGPNADAPAG 132  
Db 171 KLLGPNADAPAG 182

RESULT 14  
AAB07597  
ID AAB07597 standard; Protein; 205 AA.  
XX  
AC AAB07597;  
DT 07-NOV-2000 (first entry)  
XX  
DE A murine interleukin (IL) 173 polypeptide.  
XX  
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
KW IL-177; IL-171; cell proliferation; cancer.  
XX  
OS Mus sp.  
XX  
FH Key Location/Qualifiers  
FT Peptide 1..24 /note= "signal peptide"  
FT Protein 25..205 /note= "mature protein"  
FT Modified-site 50 /note= "phosphorylation site"  
FT Modified-site 51..53 /note= "N-glycosylation site"  
FT Modified-site 53 /note= "phosphorylation site"  
FT Modified-site 57..61 /note= "myristoylation site"  
FT Modified-site 80 /note= "phosphorylation site"  
FT Modified-site 82 /note= "phosphorylation site"  
FT Modified-site 82..84 /note= "calcium phosphorylation site"  
FT Modified-site 101..105 /note= "myristoylation site"  
FT Modified-site 113 /note= "phosphorylation site"  
FT Modified-site 116 /note= "phosphorylation site"

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FH Key Location/Qualifiers
FT Peptide 1..22
FT /label= Signal_peptide
XX
PN WO200015798-A2.
XX
PD 23-MAR-2000.
XX
PF 17-SEP-1999; 99WO-US21677.
XX
PR 17-SEP-1998; 98US-0154817.
XX
PA (ZYMO ) ZYMOGENETICS INC.
XX
PI Presnell SR, Taft DW, Foley KP;
XX
DR WPI; 2000-271436/23.
DR N-PSDB; AA252201.
XX
PT Polynucleotides encoding a novel transforming growth factor beta-9
PT polypeptide, designated ztgf beta-9, useful as an antiviral and
PT antiproliferative agent
XX
PS Claim 6; Page 92-93; 97pp; English.
XX
CC The present sequence is a variant of human transforming growth
CC factor beta-9, designated ztgf beta-9. Human ztgf beta-9 was isolated
CC from an arrayed pituitary gland cDNA plasmid library by PCR screening.
CC This can be used to treat a variety of neurodegenerative diseases such
CC as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's
CC disease, Parkinson's disease and peripheral neuropathies, or
CC demyelinating diseases including multiple sclerosis. Ztgf beta-9 peptides
CC have antiviral activity and may also be used to regulate the
CC proliferation, differentiation and apoptosis of neurons, glial cells,
CC lymphocytes, hematopoietic cells and stromal cells.
XX
SQ Sequence 209 AA;

Query Match 100.0%; Score 729; DB 21; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.6e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRFPPTNLSVSPWAYRISYDPAHYPRYLPEAYCLRCGLTGLFGEDV 60
Db 77 scpaggrrpadrrfpptnlrsvspwayrissydparyprylpeayclrcgcltglfgeedv 136

QY 61 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTIPVGTCTCVPPEKDDADSI 120
Db 137 rfrsapvymptvvlrrtpacaggrsvyteayvtipvgctcvpepekddadsinsidkqga 196

QY 121 KLLGPNDAFAGP 133
Db 197 klllgpndafagp 209

RESULT 11
AAB07594
ID AAB07594 standard; Protein; 151 AA.
XX
AC AAB07594;
XX
DT 07-NOV-2000 (first entry)
XX
DE A human interleukin (IL) 173 polypeptide.
XX
KW Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;
KW IL-177; IL-171; cell proliferation; cancer.
XX
OS Homo sapiens.
XX
PN WO200042188-A2.
XX

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PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US00006.
XX
PR 11-JAN-1999; 99US-0228822.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM, Bazan JF, Kastelein RA;
XX
DR WPI; 2000-466130/40.
DR N-PSDB; AAA58982.
XX
PT New isolated polynucleotide encoding a mammalian Interleukin-17 like
PT protein used to identify genes for homologous proteins -
XX
PS Claim 11; Page 12-13; 111pp; English.
XX
CC The present sequence represents an interleukin-173 (IL-173) polypeptide.
CC The polypeptide is an IL-17-like (CTLA-8 related) protein. It is a
CC member of a new group of interleukins IL-170 polypeptides. The members
CC comprise IL-172, IL-173, IL-174, IL-176, IL-177, and IL-171. IL-170
CC protein can be used to treat abnormal proliferation e.g. cancer
CC or degenerative conditions. Antibodies can be used in diagnostic
CC methods to detect over production of IL-170 protein in cells or body
CC fluids.
XX
SQ Sequence 151 AA;

Query Match 84.1%; Score 613; DB 21; Length 151;
Best Local Similarity 99.1%; Pred. No. 1.4e-61;
Matches 111; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRFPPTNLSVSPWAYRISYDPAHYPRYLPEAYCLRCGLTGLFGEDV 60
Db 40 scpaggrrpadrrfpptnlrsvspwayrissydparyprylpeayclrcgcltglfgeedv 99

QY 61 RFRSAPVYMTVVLRRTPACAGGRSVYTEAYVTIPVGTCTCVPPEKDDADSI 112
Db 100 rfrsapvymptvvlrrtpacaggrsvyteayvtipvgctcvpepekddadsin 151

RESULT 12
AAB07690
ID AAB07690 standard; Protein; 151 AA.
XX
AC AAB07690;
XX
DT 07-NOV-2000 (first entry)
XX
DE A rat interleukin-173 polypeptide.
XX
KW Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;
KW IL-174; IL-176; IL-177; cell proliferation; cancer.
XX
OS Rattus sp.
XX
PN WO200042187-A1.
XX
PD 20-JUL-2000.
XX
PF 10-JAN-2000; 2000WO-US00005.
XX
PR 11-JAN-1999; 99US-0229402.
XX
PA (SCHE ) SCHERING CORP.
XX
PI Gorman DM, Bazan JF, Kastelein RA;
XX
DR WPI; 2000-476060/41.
DR N-PSDB; AAA59156.
XX

```

```
XX 10-JAN-2000; 2000WO-US000005.
XX 11-JAN-1999; 99US-0229402.
XX (SCHE ) SCHERING CORP.
XX Gorman DM, Bazan JF, Kastelein RA;
XX WPI; 2000-476060/41.
XX N-PSDB; AA59155.
XX New DNA sequence encoding a mammalian homolog of CTLA-8, designated
XX interleukin-171 (IL-171), useful for recombinant production of IL-171
XX PT which can be used for treating conditions associated with abnormal
XX PT physiology or development -
XX PS Disclosure; Page 16-17; 111pp; English.
XX CC The present sequence represents an interleukin (IL)-173 polypeptide.
XX CC It is a mammalian homologue of the cytokine designated CTLA-8 (also
XX CC referred to as IL-17). The specification also describes homologues
XX CC IL-171, IL-175, IL-172, IL-173, IL-174, IL-176, and IL-177. The DNA
XX CC sequence encoding IL-171 is useful for identifying genes, mRNA and
XX CC cDNA molecules which code for related or homologous proteins. The
XX CC IL-171 protein, antibodies against IL-171, and compounds which have
XX CC binding affinity to IL-171 are useful in treatment of conditions
XX CC associated with abnormal physiology or development, including abnormal
XX CC proliferation, e.g. cancerous conditions, or degenerative conditions.
XX CC The IL-171 protein can be used in kits and assay methods for identifying
XX CC compounds that selectively bind to IL-171.
XX SQ Sequence 202 AA;
Query Match 100.0%; Score 729; DB 21; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCPAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
DB 70 scpagrpadrfrpptnlrsvspwayrissydparyprylpeayclrcgltlfgeedv 129
QY 61 RFRSAPVYMTVVLRTPACAGRSVYTEAYVTIPVGCCTCPEPEKADBSINSSIDKQGA 120
DB 130 rfrsapvymptvvlrrtpacagrsvyteayvtipvgctcvpepekdadsinssidkqga 189
QY 121 KLLGPNADAPAGP 133
DB 190 killgpnadapagp 202
RESULT 9
ID AAY70653
XX AAY70653 standard; Protein; 202 AA.
XX AC AAY70653;
XX DT 18-JUL-2000 (first entry)
XX DE Human transforming growth factor beta-9, ztgbeta-9 protein.
XX KW Human transforming growth factor beta-9; ztgbeta-9;
KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
KW antiviral; cytostatic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..15
XX PT /label= Signal_peptide
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FT Protein 16..202
XX /note= "Mature transforming growth factor beta-9"
XX WO200015798-A2.
XX PD 23-MAR-2000.
XX PF 17-SEP-1999; 99WO-US21677.
XX PR 17-SEP-1998; 98US-0154817.
XX PA (ZYMO ) ZYMOGENETICS INC.
XX PI Presnell SR, Taft DW, Foley KP;
XX WPI; 2000-271436/23.
XX DR N-PSDB; AA52195.
XX PT Polynucleotides encoding a novel transforming growth factor beta-9
XX PT polypeptide, designated ztgb beta-9, useful as an antiviral and
XX PT antiproliferative agent -
XX PS Claim 6; Page 83; 97pp; English.
XX CC The present sequence is the human transforming growth factor beta-9,
XX CC designated ztgb beta-9. Human ztgb beta-9 was isolated from an arrayed
XX CC pituitary gland cDNA plasmid library by PCR screening. This can be used
XX CC to treat a variety of neurodegenerative diseases such as amyotrophic
XX CC lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease,
XX CC Parkinson's disease and peripheral neuropathies, or demyelinating
XX CC diseases including multiple sclerosis. Ztgb beta-9 peptides have
XX CC antiviral activity and may also be used to regulate the proliferation,
XX CC differentiation and apoptosis of neurons, glial cells, lymphocytes,
XX CC hematopoietic cells and stromal cells.
XX SQ Sequence 202 AA;
Query Match 100.0%; Score 729; DB 21; Length 202;
Best Local Similarity 100.0%; Pred. No. 1.5e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SCPAGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60
DB 70 scpagrpadrfrpptnlrsvspwayrissydparyprylpeayclrcgltlfgeedv 129
QY 61 RFRSAPVYMTVVLRTPACAGRSVYTEAYVTIPVGCCTCPEPEKADBSINSSIDKQGA 120
DB 130 rfrsapvymptvvlrrtpacagrsvyteayvtipvgctcvpepekdadsinssidkqga 189
QY 121 KLLGPNADAPAGP 133
DB 190 killgpnadapagp 202
RESULT 10
ID AAY70662
XX AAY70662 standard; Protein; 209 AA.
XX AC AAY70662;
XX DT 18-JUL-2000 (first entry)
XX DE Human transforming growth factor beta-9, ztgbeta-9 variant protein.
XX KW Human transforming growth factor beta-9; ztgbeta-9;
KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;
KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;
KW peripheral neuropathy; demyelinating disease; multiple sclerosis;
KW antiviral; cytostatic.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..15
XX PT /label= Signal_peptide
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Qy 61 RFRSAPYVMTVLRRTTPACAGRSVYTEAYVTIPVGCCTVPEPEKADSDINSIDKQGA 120  
 |||  
 Db 115 rfrsapymptvrrrrtpacagrsvsyateayvtipvgctcvpepekdadsinsidkqga 174  
 |||  
 Qy 121 KLLGPNADAPAGP 133  
 |||  
 Db 175 klllgpnadapagp 187

RESULT 7  
 AAB07595  
 ID AAB07595 standard; Protein; 202 AA.  
 AC AAB07595;  
 XX  
 XX 07-NOV-2000 (first entry)  
 DT  
 DE A human interleukin (IL) 173 polypeptide.  
 XX  
 XX Interleukin; IL-17; CTLA-8; IL-170; IL-172; IL-173; IL-174; IL-176;  
 KW IL-177; IL-171; cell proliferation; cancer.  
 KW  
 XX Homo sapiens.  
 OS

Key Peptide Location/Qualifiers  
 1..17 /note= "signal peptide"  
 FT  
 FT Protein 18..202 /note= "mature protein"  
 FT  
 FT Modified-site 50 /note= "phosphorylation site"  
 FT  
 FT Modified-site 50..53 /note= "CAMP protein kinase phosphorylation site"  
 FT  
 FT Modified-site 53 /note= "phosphorylation site"  
 FT  
 FT Modified-site 57..61 /note= "myristoylation site"  
 FT  
 FT Modified-site 57..61 /note= "myristoylation site"  
 FT  
 FT Modified-site 66..69 /note= "CAMP protein kinase phosphorylation site"  
 FT  
 FT Modified-site 66..69 /note= "CAMP protein kinase phosphorylation site"  
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 FT Modified-site 72..75 /note= "CAMP protein kinase phosphorylation site"  
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 FT Modified-site 72..75 /note= "CAMP protein kinase phosphorylation site"  
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 FT Modified-site 72 /note= "phosphorylation site"  
 FT  
 FT Modified-site 75 /note= "phosphorylation site"  
 FT  
 FT Modified-site 80 /note= "phosphorylation site"  
 FT  
 FT Modified-site 82 /note= "phosphorylation site"  
 FT  
 FT Modified-site 82..84 /note= "calcium phosphorylation site"  
 FT  
 FT Modified-site 113 /note= "phosphorylation site"  
 FT  
 FT Modified-site 113..116 /note= "CAMP protein kinase phosphorylation site"  
 FT  
 FT Modified-site 113..116 /note= "CAMP protein kinase phosphorylation site"  
 FT  
 FT Modified-site 116 /note= "phosphorylation site"  
 FT  
 FT Modified-site 164..166 /note= "myristoylation site"  
 FT  
 FT Modified-site 164..166 /note= "myristoylation site"  
 FT  
 FT Modified-site 166..168 /note= "calcium phosphorylation site"  
 FT  
 XX WO200042187-A1.  
 PN  
 XX 20-JUL-2000.

Db 130 rfrsapymptvrrrrtpacagrsvsyateayvtipvgctcvpepekdadsinsidkqga 189  
 Qy 121 KLLGPNADAPAGP 133  
 |||  
 Db 190 klllgpnadapagp 202

RESULT 8  
 AAB07689  
 ID AAB07689 standard; Protein; 202 AA.  
 XX  
 AC AAB07689;  
 XX  
 XX 07-NOV-2000 (first entry)  
 DT  
 DE A human interleukin-173 polypeptide.  
 XX  
 KW Interleukin; IL-171; cytokine; CTLA-8; IL-17; IL-175; IL-172; IL-173;  
 KW IL-174; IL-176; IL-177; cell proliferation; cancer.  
 KW  
 XX Homo sapiens.  
 OS

Key Peptide Location/Qualifiers  
 1..17 /note= "signal peptide"  
 FT  
 FT Protein 18..202 /note= "mature protein"  
 FT  
 FT Modified-site 50 /note= "phosphorylation site"  
 FT  
 FT Modified-site 50..53 /note= "CAMP protein kinase phosphorylation site"  
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 FT Modified-site 53 /note= "phosphorylation site"  
 FT  
 FT Modified-site 57..61 /note= "myristoylation site"  
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 FT Modified-site 57..61 /note= "myristoylation site"  
 FT  
 FT Modified-site 66..69 /note= "CAMP protein kinase phosphorylation site"  
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 FT Modified-site 82 /note= "phosphorylation site"  
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 FT Modified-site 82..84 /note= "calcium phosphorylation site"  
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 FT Modified-site 164..166 /note= "myristoylation site"  
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 FT  
 FT Modified-site 166..168 /note= "calcium phosphorylation site"  
 FT  
 XX WO200042187-A1.  
 PN  
 XX 20-JUL-2000.

Query Match 100.0%; Score 729; DB 21; Length 202;  
 Best Local Similarity 100.0%; Pred.No. 1.5e-74;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 SCPAGGPADRRPPTNLRSPVSWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEDV 60  
 |||  
 Db 70 scpaggpadrfrprrpntlrsvspwayrissydparyprylpeayclrcgltglfgeedv 129  
 |||  
 Qy 61 RFRSAPYVMTVLRRTTPACAGRSVYTEAYVTIPVGCCTVPEPEKADSDINSIDKQGA 120  
 |||

QY 1 SCPAGGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60  
 Db 54 scpaggrpadrrfrpntnrlsrspwayrissydparyprylpeayclrcgltlfgeedv 113  
 QY 61 RFRSAPVYMPVTLRTPACAGRSVYTYAYVTPVGCCTCVPEPEKADDSINSSIDKQGA 120  
 Db 114 rfrsapvymptvllrrtpacagrsvytyayvtipvgctcvpepekadsinssidkqga 173  
 QY 121 KLLGPNDAAPG 133  
 Db 174 kllgpnadapagp 186

RESULT 5  
 AAY70654  
 ID AAY70654 standard; Protein; 187 AA.  
 XX  
 AC AAY70654;  
 XX  
 DT 18-JUL-2000 (first entry)  
 XX  
 DE Mature human transforming growth factor beta-9, Ztgbeta-9 protein-1.  
 XX  
 KW Human transforming growth factor beta-9; Ztgb beta-9;  
 KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;  
 KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;  
 KW peripheral neuropathy; demyelinating disease; multiple sclerosis;  
 KW antiviral; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200015798-A2.  
 XX  
 PD 23-MAR-2000.  
 XX  
 PF 17-SEP-1999; 99WO-US21677.  
 XX  
 PR 17-SEP-1998; 98US-0154817.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Presnell SR, Taft DW, Foley KP;  
 XX  
 DR WPI; 2000-271436/23.  
 DR N-PSDB; AA252195.  
 XX  
 PT Polynucleotides encoding a novel transforming growth factor beta-9  
 PT polypeptide, designated Ztgb beta-9, useful as an antiviral and  
 PT antiproliferative agent  
 XX  
 PS Claim 6; Page 84; 97pp; English.

The present sequence is the mature human transforming growth factor beta-9, designated Ztgb beta-9. This is a mature sequence excluding the signal sequence extending from amino acid 16 to and including amino acid 202 of Ztgb beta-9. Human Ztgb beta-9 was isolated from an arrayed pituitary gland cDNA library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Ztgb beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.

Query Match 100.0%; Score 729; DB 21; Length 187;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-74;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60  
 Db 55 scpaggrpadrrfrpntnrlsrspwayrissydparyprylpeayclrcgltlfgeedv 114  
 QY 61 RFRSAPVYMPVTLRTPACAGRSVYTYAYVTPVGCCTCVPEPEKADDSINSSIDKQGA 120  
 Db 115 rfrsapvymptvllrrtpacagrsvytyayvtipvgctcvpepekadsinssidkqga 174  
 QY 121 KLLGPNDAAPG 133  
 Db 175 kllgpnadapagp 187

RESULT 6  
 AAY70663  
 ID AAY70663 standard; Protein; 187 AA.  
 XX  
 AC AAY70663;  
 XX  
 DT 18-JUL-2000 (first entry)  
 XX  
 DE Mature human Ztgbeta-9 variant protein.  
 XX  
 KW Human transforming growth factor beta-9; Ztgb beta-9;  
 KW Alzheimer's disease; neurodegenerative disease; Huntington's disease;  
 KW amyotrophic lateral sclerosis; ALS; Parkinson's disease;  
 KW peripheral neuropathy; demyelinating disease; multiple sclerosis;  
 KW antiviral; cytostatic.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200015798-A2.  
 XX  
 PD 23-MAR-2000.  
 XX  
 PF 17-SEP-1999; 99WO-US21677.  
 XX  
 PR 17-SEP-1998; 98US-0154817.  
 XX  
 PA (ZYMO ) ZYMOGENETICS INC.  
 XX  
 PI Presnell SR, Taft DW, Foley KP;  
 XX  
 DR WPI; 2000-271436/23.  
 DR N-PSDB; AA252201.  
 XX  
 PT Polynucleotides encoding a novel transforming growth factor beta-9  
 PT polypeptide, designated Ztgb beta-9, useful as an antiviral and  
 PT antiproliferative agent  
 XX  
 PS Claim 6; Page 93-94; 97pp; English.

The present sequence is a mature variant human transforming growth factor beta-9 protein, designated Ztgb beta-9. Human Ztgb beta-9 was isolated from an arrayed pituitary gland cDNA library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Ztgb beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.

Query Match 100.0%; Score 729; DB 21; Length 187;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-74;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SCPAGGRPADRRPPTNLRSPWAYRISYDPARYPRYLPEAYCLRCGLTGLFGEEDV 60  
 Db 55 scpaggrpadrrfrpntnrlsrspwayrissydparyprylpeayclrcgltlfgeedv 114

Best Local Similarity 100.0%; Pred. No. 1.2e-74;  
Matches 133; Conservative 0; Mismatches 0;

[illegible]

RESULT 3  
AAY70656  
ID AAY70656 standard; Protein: 185 AA.

AA	AAY70656;
AC	
XX	18-JUL-2000 (first entry)
DT	
XX	
DE	Mature human transforming growth factor beta-9, Ztgfbeta-9 protein-3.
XX	
KW	Human transforming growth factor beta-9; Ztgf beta-9;
KW	Alzheimer's disease; neurodegenerative disease; Huntington's disease;
KW	amyotrophic lateral sclerosis; ALS; Parkinson's disease;
KW	peripheral neuropathy; demyelinating disease; multiple sclerosis;
KW	antiviral; cytostatic.

OS	Homo sapiens.
XX	
PN	WO200015798-A2.
XX	
XX	
PD	23-MAR-2000.
XX	
PF	17-SEP-1999;
XX	99WO-US21677.
XX	
PR	17-SEP-1998;
	98US-0154817.

XX PA (ZYMO ) ZYMOGENETICS INC.  
XX PI  
XX Presnell SR, Taft DW, Foley KP;  
DR WPI; 2000-271436/23.  
DR N-PSDB; AAZ52195.

XX Polynucleotides encoding a novel transforming growth factor beta-9  
 PT polypeptide, designated ztgf beta-9, useful as an antiviral and  
 PT antiproliferative agent -  
 XX  
 PS Claim 6; Page 85-86; 97pp: English.

The present sequence is the mature human transforming growth factor beta-9, designated Tgfb beta-9. This is a mature sequence excluding the signal sequence extending from amino acid 18 to and including amino acid 202 of Tgfb beta-9. Human Tgfb beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Tgfb beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.

AA	Sequence	185 AA;
SQ		

Query Match	100.0%;	Score 729;	DB 21;	Length 185;
Best Local Similarity	100.0%;	Pred. No. 1.3e-74;		

```
Best Local Similarity 100.0%; Pred. No. 1.2e-74;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	scpaggrrpadrrfppnlrksrsvswainrksrtdparyrprlpea	clcrkcgtlgtfgedv	60
Db	53	scpaggrrpadrrfippnlrsvspwayrsvdypryprlpeaycl	rgclgtfgedv	112
Qy	61	rfrsapvymptvvlrrrrpacaggrsvtveayvtipvgctcv	pepekdadsinsstdkoga	120
Db	113	rfrsapvymptvvlrrtpacaggrsvtveayvtipvgctcv	pepekdadsinsidkaga	172
Qy	121	klldgpnadapagp	133	
Db	173	klldgpnadapagp	185	

RESULT 4  
AAY70655  
ID AAY70655 standard; Protein; 186 AA.

AC	AA70655;
XX	
XX	18-JUL-2000 (first entry)
Dr	
XX	
DE	Mature human transforming growth factor beta-9, ztgbeta-9 protein-2.
XX	
XX	
KW	Human transforming growth factor beta-9; ztgf beta-9;
KW	Alzheimer's disease; neurodegenerative disease; Huntington's disease;
KW	amyotrophic lateral sclerosis; ALS; Parkinson's disease;
KW	peripheral neuropathy; demyelinating disease; multiple sclerosis;
KW	antiviral; cytostatic.
KW	

AA	Homo sapiens.
OS	
XX	WO200015798-A2.
PN	
XX	23-MAR-2000.
PD	
XX	17-SEP-1999;
PF	99WO-US21677.
XX	
PR	17-SEP-1998;
XX	98US-0154817.

PA (ZYMO) ZYMOGENETICS INC.

PI Presnell SR, Taft DW, Foley KP;

AA WPI; 2000-271436/23.  
DR N-PSDB; AAZ52195.  
DR

AA Polynucleotides encoding a novel transforming growth factor beta-9  
PT polypeptide, designated 2tgf beta-9, useful as an antiviral and  
PT antiproliferative agent -

PS Claim 6; Page 84; 97pp; English.

The present sequence is the mature human transforming growth factor beta-9, designated Tgfb beta-9. This is a mature sequence excluding the signal sequence extending from amino acid 17 to and including amino acid 202 of Tgfb beta-9. Human Tgfb beta-9 was isolated from an arrayed pituitary gland cDNA plasmid library by PCR screening. This can be used to treat a variety of neurodegenerative diseases such as amyotrophic lateral sclerosis (ALS), Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases including multiple sclerosis. Tgfb beta-9 peptides have antiviral activity and may also be used to regulate the proliferation, differentiation and apoptosis of neurons, glial cells, lymphocytes, hematopoietic cells and stromal cells.

AA	Sequence	186 AA:
SQ		

Query Match	100.0%;	Score 729;	DB 21;	Length 186;
Best Local Similarity	100.0%;	Pred. No. 1:3e-74;		
Matches 133; Conservative	0;	Mismatches	0;	Indels



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 5, 2001, 15:19:50 ; Search time 21.13 Seconds  
(without alignments)  
381.590 Million cell updates/sec

Title: US-09-320-713-4\_COPY\_28\_160  
Perfect score: 729  
Sequence: 1 SCPAGGRPADRRFRPTNLR.....SIDKQAKLLGPNAPAGP 133

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 50623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_0601.\*  
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2: /SID88/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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22: /SID88/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	729	100.0	160	21	AAV53891
2	729	100.0	173	21	AAV53893
3	729	100.0	185	21	AAV70856
4	729	100.0	186	21	AAV70855
5	729	100.0	187	21	AAV70654
6	729	100.0	187	21	AAV70663
7	729	100.0	202	21	AAV70595
8	729	100.0	202	21	AAV70689
9	729	100.0	202	21	AAV70653
10	729	100.0	209	21	AAV70662
11	613	84.1	151	21	AAV70594

12	613	84.1	151	21	AAV70690	A rat interleukin-
13	601	82.4	183	21	AAV70658	Mature murine tran
14	601	82.4	205	21	AAV70597	A murine interleuk
15	601	82.4	205	21	AAV70691	A murine interleuk
16	601	82.4	205	21	AAV70657	Murine transformin
17	354	48.6	103	21	AAV70688	A human interleuki
18	303	41.6	57	21	AAV70666	Human transforming
19	242	33.2	54	21	AAV70664	Human transforming
20	208	28.5	44	21	AAV70596	A rat interleukin
21	193	26.5	425	21	AAV44462	Human interleukin
22	187.5	25.7	197	21	AAV18911	A novel polypeptid
23	187.5	25.7	197	21	AAV70602	A human interleuki
24	187.5	25.7	197	21	AAV70684	A human interleuki
25	187.5	25.7	197	21	AAV92238	Human interleukin-
26	187.5	25.7	197	21	AAV44460	Human interleukin
27	187.5	25.7	197	21	AAV53892	Amino acid sequenc
28	187.5	25.7	206	21	AAV44485	Human interleukin
29	180	24.7	34	21	AAV70661	Human transforming
30	176.5	24.2	408	21	AAV44461	Human interleukin
31	174	23.9	128	21	AAV85643	Human 2cyto7 matur
32	174	23.9	130	21	AAV93975	Amino acid sequenc
33	174	23.9	151	20	AAV85641	Human 2cyto7 matur
34	174	23.9	153	20	AAV85642	Human 2cyto7 matur
35	174	23.9	154	20	AAV85640	Human 2cyto7 matur
36	174	23.9	157	20	AAV85644	Human 2cyto7 matur
37	174	23.9	158	20	AAV85639	Human 2cyto7 matur
38	174	23.9	160	20	AAV85618	Human 2cyto7 matur
39	174	23.9	160	20	AAV85619	Human 2cyto7 matur
40	174	23.9	160	20	AAV85620	Human 2cyto7 matur
41	174	23.9	160	20	AAV85621	Human 2cyto7 matur
42	174	23.9	160	20	AAV85622	Human 2cyto7 matur
43	174	23.9	160	20	AAV85626	Human 2cyto7 matur
44	174	23.9	160	20	AAV85627	Human 2cyto7 matur
45	174	23.9	160	20	AAV85628	Human 2cyto7 matur

ALIGNMENTS

RESULT 1	
AAV53891	AAV53891 standard; Protein: 160 AA.
ID	AAV53891
XX	AC AAV53891;
XX	DP 13-MAR-2000 (first entry)
XX	DE Partial amino acid sequence of human interleukin-22.
XX	Human; interleukin-22; IL-22; IL-21; immune system disorder;
KW	immune cell chemotaxis; haematopoietic cell disorder;
KW	haemostatic activity; thrombolytic activity; autoimmune disorder; asthma;
KW	respiratory problem; organ rejection; graft-versus-host disease; GVHD;
KW	inflammation; hyperproliferative disorder; tissue regeneration;
KW	embryonic stem cell differentiation; embryonic stem cell proliferation;
KW	haematopoietic lineage; allergic asthma.
XX	OS Homo sapiens.
XX	Key Location/Qualifiers
FT	Modified-site 26
FT	/note= "potential N-linked glycosylation site"
FT	Domain 57..64
FT	/note= "conserved domain I"
FT	Domain 72..77
FT	/note= "conserved domain II"
FT	Domain 99..105
FT	/note= "conserved domain III"
FT	Domain 121..128
FT	/note= "conserved domain IV"
FT	Modified-site 139
FT	/note= "potential N-linked glycosylation site"
XX	